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Result
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Maximum DB
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Perfect score:
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1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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9: /SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
10: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
11: /SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
12: /SIDSB/gcgdata/geneseq/geneseqp/AA1992.DAT:*
13: /SIDSB/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
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18: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
19: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
20: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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Match
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100.0
100.0
100.0
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91.2
91.2
90.3
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Gapop 10.0 ,
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1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen
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d by analysis of the total
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              668
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746
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937
937
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             AAW76391
AAR36808
AAR32456
AAR32456
AAR36810
AAR36809
AAR36809
AAR36809
AAR36809
 AAR32455
                                                                                                                                                                                                               SUMMARIES
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                                                                                                                                                                                                                                           score distribution
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412676
                       Pseudomonas aerugi
Pseudomonas Exotox
PE with inactivate
PE having M1 resid
Full-length PE wit
PE having M1 resid
Full-length PE wit
PE binding/translo
PE binding and tra
                                                                                                                                                           Description
Pseudomonas exc
Ps amino acids
 RESULT
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                                                                                                                            Domain
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                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                  Pseudomonas
                                                                                                                                                                                                                                                                                                                             Exotoxin
                                                                                                                                                                                                                                                                                                                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                AAW76391;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW76391 standard; Protein; 638
                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                             A;
                                                                                                                                                                                                                                                                                                 aeruginosa.
                                                                                                                                                                                                                                                                                                                                                       aeruginosa exotoxin
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                            405..613
                                                                                                                                                                                                              253..364
                                                                                                                                                                                                  /label= II
                                                                                                                                                                                                                                          /label=
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IL-13 binding chai	529	21	380	6.7	88
Construct containi	AAW56260	19	359	٠	88
	AAW56261	19	315		88
Ď,	AAP82349	9	16	٠	91
	AAW46771	19	~1		1.3
acid seque	AAW46761	19	1684		93.5
prote	AAW25671	18	•	٠	1.1
Amino acid sequenc	AAB07463	21	25	9.7	128
A chimeric toxin c	AAY43545	20	635		1181
Aa mutant chimeric	AAY43547	20	634	89.3	1181
Pseudomonas exotox	AAR40112	14	613	89.7	1187
Pseudomonas exotox	AAR40109	14	613		1187
Pseudomonas exotox	AAR40104	14	613	•	1187
S	AAR40111	14	613		9
	AAR40110	14	613		1190
Pseudomonas exotox	AAR40108	14	613		1190
Pseudomonas exotox	AAR40107	14	613		1190
Pseudomonas exotox	AAR40106	14	613		1190
Pseudomonas ex	AAR40105	<u>1</u> 4	613	•	1190
PE binding	AAR32469	14	917		1195
PE binding/	AAR36821	14	917		1195
BSPEM1c5aa fragmen	AAR32468	14	670		1195
PE-Influenza A vir	AAR36820	14	670		1195
PE(2-414)-M1(2-252	AAR32453	14	665		1195
Pseudomonas exotox	AAR36805	14	665	90.3	1195
e pseu	AAR87738	16	614		1195
sequen	AAB07462	21	613		1195
sp.	AAW92912	20	613		1195
sp. e	$\sim$	20	613		1195
	27	19	613		1195
	11	14	613	٠	1195
eudomonas exoto	$\vdash$	14	613		1195
(2-414)-Ma(57-6	24	14	426	90.3	1195
PE domains I and I	AAR36806	14	426		1195

## ALIGNMENTS

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01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETA; toxA gene; drug delivery; membrane transport
                                                                                                                        /note= "enzymatic ADP-ribosylation domain"
634..638
                                                                                                                                                                                                                                                       /note= "membrane 365..404
                                                                                                                                                                                                           /label= I
/note= "receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        note- "receptor binding domain"
                                                                                "peptide important for intracellular
transport and cytotoxicity of ETA"
                                                                                                                                                                                                                                                                           penetrating domain"
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RESULT
AAR36808
                                                                                                                                                                                                                                                                                                           QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exotoxin A (ETRA), a virulence factor and secreted protein encoded CC by the toxA gene (see AAV61784). The invention employs a group of CC membrane penetrating proteins, of which ETA is an example, to CC carry a variety of therapeutic agents across the cellular membrane CC carry a variety of therapeutic agents across the cellular membrane CC card, peptide, peptide nucleic acid, (single chain) antibody, or CC control of a enkaryotic promoter (e.g. the cytomegalovirus control of a enkaryotic promoter (e.g. the cytomegalovirus control of a enkaryotic promoter (e.g. the cytomegalovirus conding protein, single chain antibody, tumour suppressor, it CC encodes an antisens molecule that targets an oncogene or viral CC encodes an antisense molecule that targets an oncogene or viral CC ertaining its ability to transport molecules across membranes, or CC by introduction of a free cysteine in domain III (see AAW61787). CC conjugates of ETA, specifically apptide nucleic acids (see AAW61787). CC conjugates of ETA, specifically peptide nucleic acids (see AAW61787). CC administered, thereby reducing toxicity, and provide effective targetting of an agent to a specific point within a cell.
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Best Local S
Matches 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-532023/45
N-PSDB; AAV61784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TEXA ) UNIV TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
AAR36808;
                             AAR36808 standard;
                                                                                                     241
                                                                                                                                241
                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                        SWSLNWLVPIGHEKPSNIKVFIHELNAGNOLSHMSPIYTIEMGDELLAKLARDATFFVRA 180
                                                                                                                                                                                                                                                                                \tt dtngqgvlhysmvleggndalklaidnalsitsdgltirleggvepnkpvrysytrqarg
                                                                                                                                                                                                                                                                                              DTNGGGVLHYSNYLEGGNDALKLAIDNALSITSDGITIRLEGGVEPNKPVRYSYTROARG 120
                                                                                                                                                           LDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 58-60; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0042056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US05710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM
                                                                                                       252
                             Protein; 652
                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1323; DB 19; 100.0%; Pred. No. 2.2e-129; tive 0; Mismatches 0;
                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                      638;
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                                                                                                                                                                                      Matches
                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; matrix protein; Ma; cell recognition domain; translocati ADP-ribosylating domain; anti-viral agent.
                                                                                                                                                                                                                                                           Plasmid pVCPE/2 was made by replacing the 105bp PpuMI/EcoRI fragment of pVC45DF+T (containing the Pseudomonas Exotoxin coding region) with a 46bp DNA fragment (AAQ41718) encoding an in-frame duplication of PE codons 604 to 613 flanked by unique restriction sites. This construct is used for generating full-length molecules of PE with the deletion of residue 553 resulting in an inactivated toxin domain (AAQ41719) fused to chosen protein segments between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-154266/19.
N-PSDB; AAQ41719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP541335-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                      Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Donnelly JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1993
                                                                                                                                                                                                                                                                                                                                     Example 7; Page 34-37;
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                     PE codons
241
                 241
                                     181
                                                                         121
                                                                                           121
                                                       181
                                                                                                             61
                                                                                                                                61
                                                                                                                                                                                               Local Similarity
                                                                                                                                                lddtwegkiyrv
                  LDDTWEGKIYRV 252
                                                                                                                                                                                                                                                    604 and 605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exotoxin with inactivated
                                                                                                                                                                                                                                    652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aeruginosa
                                                                                                                                                                                     100.0%; Score 1323; DB 14; ilarity 100.0%; Pred. No. 2.3e-129; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   & CO
                                                                                                                                                                                                                                                                                                                                                                                                                        Friedman A,
, Oliff AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0792507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92EP-0310067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
 252
                                                                                                                                                                                                                                                                                                                                       81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Hawe LA,
Shi X, (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nonsense codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                   Marshall MS
                                                                                                                                                                                          Indels
                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain;
                                                                                                                                                                                          0
                                                                                                                                                                                         Gaps
                                                           240
                                                                                               180
                                                                                                                                    120
                                        240
                                                                              180
                                                                                                                 120
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0

Synthetic.

AAR32456;

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Example 8 describes the construction of pVCPE/2-Ma. pVCPE/2-Ma was made by ligating into the XmaI site of pVCPE/2 a 48 base pair DNA fragment encoding amino acids 55 through 67 (AAQ36020). This construct expresses in E.coli full-length PE with MI amino acids 55 through 67 inserted between PE amino acids 604 and 605 (AAQ38394). One may replace the ompA signal sequence with the promoter/ribosome binding site as described for pVC-PEMI-2.
swslnwlvpighekpsnikvfihelnagnqlshmspiytiemgdellaklardatffvra 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHLIPHWIPLVASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA 60
                                                          /note- "residue not defined in the specification; encoded by stop codon TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residues 55 through 67 between residues 604 and 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion; hybrid; pVCPE/2-Ma; pVC-PEM1-2; ompA; signal sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial toxin-antigen protein conjugates - to elicit (
T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1323; DB 14; 100.0%; Pred. No. 2.3e-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 40-42; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter; ribosome binding site; RBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              наме ГА,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       AAR32457 standard; Protein; 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-0756249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92EP-0202660
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Oliff AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    & CO INC
                                                                                                                                                                      LDDTWEGKIYRV 252
                                                                                                                                                                                                      WPI; 1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR32457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Donnelly JJ, F. Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          having M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAR32457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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     121
                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                               AAR32457
                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                              NAMES OF A STATE OF A 
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pVCPE/2 was made by replacing the 105 base pair PpuMI/ECORI
fragment of pVC45DF+T with a 46 base pair DMA fragment encoding an
inframe duplication of PE codons 604 to 613 flanked by unique cloning
sites. This construct is used for generating full-length mols. of PE
with the deletion of residue 553 resulting in an activated toxin
domain (AAQ36019) fused to protein segments of choice between PE
codons 604 and 605. One may replace the ompA signal sequence
with the promoter/ribosome binding site as described for pVC-PEMI-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWSLMWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DINGQCVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MHLIPHWIPLVASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "residue not defined in the specification; encoded by stop codon TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                                                                                            PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; flusion; hybrid; pvC45DF+T/2; pvC4-PEM1-2; duplication; ompa; signal sequence; promoter; ribosome binding site; RBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marshall MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1323; DB 14;
Pred. No. 2.3e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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100.0%; Pred. No. z...
'... 0; Mismatches
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t, Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; Page 78 + 37-40; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hawe LA,
Shi X,
                                                                                 AAR32456 standard; Protein; 652 AA.
                                                                                                                                                                                                                                                        PE with inactivated toxin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92EP-0202660
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                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Friedman A,
, Oliff AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.
Best Local Similarity 100.
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-087107,
N-PSDB; AAQ36019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
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Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1992;
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Sequence

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Marshall MS;

, Liu MA, Ulmer J;

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Gaps

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Indels

Length 668;

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EP532090-A.
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AAR32458
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            180
DINGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pVCPE/1-MI:15-106 was made by subcloning a PCR-amplified DNA fragment encoding MI amino acids 15 to 106 into the XmaI site of pVCPE/2 (see AAQ41718). The primers used in the amplification reaction had sequences AAQ41722 and AAQ41723. The construct express in E.coli full-length PE with MI amino acids 15-106 inserted between PE amino acid 604 and 605 (see AAQ41724).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful as vaccines against viral infections, tumours and parasites
                                          SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA
                                                   181 HESNEMQPTLAISHAGVSVVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN
                                                                                              PE with Influenza A virus MI codons 15-106 inserted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marshall MS;
                                                                                                                                                                                                                                                                                            influenza A virus;
                                                                                                                                                                                                                                                                                          Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus
matrix protein; anti-viral agent; Pseudomonas exotoxin.
                                                                                                                                                                                                                                                                                                                                                                      744
/note= "corresponds to nonsense codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Liu MA,
Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Page 45-47; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hawe LA,
Shi X, U
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                         AAR36810 standard; Protein; 746 AA
                                                                                                                                                                                                                                                                                                                            Chimeric Pseudomonas aeruginosa Chimeric Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              92EP-0310067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0792507
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedman A,
Oliff AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERI ) MERCK & CO INC.
                                                                                                                                241 LDDTWEGKIYRV 252
                                                                                                                                            241 lddtwegkiyrv 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-154266/19.
N-PSDB; AAQ41724.
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                                                                                                                                                                                                                                                                                                                                                              Key
Misc-difference
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Montgomery DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-1991;
                                                                                                                                                                                                                                                    25-AUG-1993
                                                                                                                                                                                                                                                                          Full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Gaps

0;

Indels

100.0%; Score 1323; DB 14; 11arity 100.0%; Pred. No. 2.8e-129; Conservative 0; Mismatches 0; 1

Query Match Best Local Similarity Matches 252; Conserv

Length 746;

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Example 9 describes the construction of pVCPE/2-M1:15-106. pVCPE/2-M1:15-106 was made by subcloning a PCR-amplified DNA fragment encoding M1 amino acids 15 through 106 into the Xmal site of pVCPE/2. The sequence of the oligonucleotide primers used to amplify the M1 segment are those shown in AAQ38395-96, respectively. This construct expresses in E.coli full length PE with M1 amino acids 15 through 106 inserted between PE amino acids 604 and 605 (AAQ38397).
                                                                                                                                                         240
                                                                                                                                                                    120
                                                                                                      180
                                                                                                                  120
                        9
                                                                                                                                                                                                                                                                                                                                                                                                           PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion; hybrid; pVCPE/2-M1:15-106; pVCPE/2; ompA; signal sequence; promoter; ribosome binding site; RBS; primer; PCR; amplification.
DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG
                                                                SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA
                                                                                                                                                         181 HESNEMQPTLAISHAGVSVVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN
                                                                                                                                                                                                                                                                                                                                                                                PE having M1 residues 15 through 106 between residues 604 and 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "residue not defined in the specification;
encoded by stop codon TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marshall MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial toxin-antigen protein conjugates - to elicit in lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Liu l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 48-50; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĽĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                         AAR32458 standard; Protein; 746 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hawe LA
Shi X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92EP-0202660.
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, Oliff AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                 241 LDDTWEGKIYRV 252
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N-PSDB; AAQ38397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference
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Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-SEP-1992;
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RESULT
AAR36809
ID AAR3
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Query Match
Best Local
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                useful as
parasites
                                                                                                                                                                                                Key
Misc-difference
                                                                                                                                                                                                                                                    Vaccine; cytotoxic T lymphocyte; CTL; influer matrix protein; Ma; cell recognition domain; ADP-ribosylating domain; anti-viral agent.
                                                                                                                                                                                                                                                                                                                                           AAR36809 standard; Protein; 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One may replace the ompA signal sequence with the promoter/ribosome binding site as described for pVC-PEM1-2.
                                                                                                                      08-NOV-1991;
                                                                                                                                        04-NOV-1992;
                                                                                                                                                                                                                                                                                       Full-length PE with Influenza virus MI fragment inserted
                                                                                                                                                                                                                                                                                                       25-AUG-1993
                                                                                                                                                                                                                                                                                                                         AAR36809;
                                                                                                                                                                                                                             Chimeric
Example 8; Page 36-42; 81pp; English
                        Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                           Donnelly JJ,
Montgomery DL,
                                                                                                                                                         12-MAY-1993
                                                                                                     (MERI ) MERCK & CO INC
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                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDDTWEGKIYRV 252
|||||||||||
||1ddtwegkiyrv 252
                                                          1993-154266/19.
                                                                                                                                                                                                                                                                                                                                                                                                                     HESNEMOPTLAISHAGVSVVMAQTOPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                           Pseudomonas aeruginosa
Influenza A Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         746 AA;
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                            Friedman A,
, Oliff AA,
                                                                                                                      91US-0792507.
                                                                                                                                        92EP-0310067
                                                                                                                                                                                                  Location/Qualifiers 666
                                                                                                                                                                                         /note- "corresponds to nonsense codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.6%;
                                                                            Hawe
Shi x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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                                                                                                                                                                                                                                                             influenza A virus;
domain; translocation
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                                                                                    Marshall
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                                                                                                                                                                                                                                                              domain;
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RRESULT
AAR3682
ID AAR2
XX AAR3
AC AAR2
XX VACC
DT 25-A
DT 25-A
DT 25-A
XX VACC
Chin
XX Chin
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pVCPE/2-Ma was made by ligating into the XmaI site of pVCPE/2 (see AAQ41718) a 48bp DNA fragment encoding amino acids 67 of Influenza A virus. The resulting construct expresses in E full-length PE with MI amino acids 55-67 inserted between PE ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid 604 and 605 (see AAQ41721).
                                                                                                                                                         WPI; 1993-154266/19.
N-PSDB; AAQ41731.
                                                                                                                                                                                                                            Donnelly JJ,
Montgomery D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; cytotoxic T lymphocyte; CTL; Human Immunodeficiency Virus; AIDS; anti-viral agent; Pseudomonas exotoxin; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR36822 standard;
                                                                  parasites
                                                                                                            Recombinant DNA encoding
                                                                                                                                                                                                                                                                                                                                           08-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PE binding/translocation domains-HIV gag fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-1993 (first entry)
                                                                                         useful as vaccines
                                                                                                                                                                                                                                                                                            (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dtngqgvlhysmvleggndalklaidnalsitsdgltirleggvepnkpvrysytrqarg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Immunodeficiency Virus. Pseudomonas aeruginosa.
                                                                                                                                                                                                                            DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             668 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                            Friedman A,
                                                                                                                                                                                                                                                                                                                                             91US-0792507
                                                                                                                                                                                                                                                                                                                                                                                        92EP-0310067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
                                                                                     coding bacterial toxin-antigen conjugates against viral infections, tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%;
                                                                                                                                                                                                                            Hawe LA,
Shi X, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      937
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Pred. No. 5.3e-128;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                            Ulmer J;
                                                                                                                                                                                                                                                   Marshall MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 668;
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                                                                                                               are
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Example

26; Page 70-74;

81pp;

English

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RESULT
AAR32470
ID AAR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A fragment containing the HIV gag gene was obtained from plasmid HIVPBR322 by PCR with primers that added a SacII site adjacent to the ATG codon of gag (to give the sequence AAQ41729), and a SacI simmediately after the termination codon at the 3' end (to give the sequence AAQ41730). The PCR fragment was cloned into plasmid pvc45DF+7 (containing Pseudomonas Exotoxin sequence). In the resulting plasmid, pVC-ompA-PEGAG, the binding and translocation domains of PE were fused to the gag gene of HIV-1. The fusion contains an own leader.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                             PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion; hybrid; pVC-ompA-PEGAG; HIV-1; HIVpBR322; pVC45DF+T; PCR; amplification; binding; translocation; domain;
                                                                                                                                                                                                                                                                                          PE binding
                                                                                                                                                                                                                                                                                                                                                           AAR32470 standard; Protein; 937 AA.
                                                                                        Montgomery DL,
                                                                                                   Donnelly JJ,
                                                                                                                         (MERI ) MERCK & CO INC.
                                                                                                                                                                     02-SEP-1992;
                                                                                                                                                                                          17-MAR-1993
                                                                                                                                                                                                                                                                                                                20-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  250
                                                                                                                                                                                                                                                                                                                                                                                                                                       251
                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPI 130
                                                                                                                                                                                                                                                                                                                                                                                                                  rv 251
                                                                    1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                     RV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231;
                                                          AAQ38414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an ompå leader.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             937
                                                                                                                                                                                                                                                                                           and translocation domains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                         Friedman A,
,, Oliff AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                               91US-0756249
                                                                                                                                                                     92EP-0202660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%;
95.5%;
                                                                                         Hawe LA,
Shi X, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1207; DB 14; Pred. No. 5e-117;
                                                                                          A, Liu
Ulmer
                                                                                                                                                                                                                                                                                             HIV GAG fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                      Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 10
AAR3680
XX AAR368
XX AAR368
XX Pseudo
XX Vaccin
KW Wacrin
KW Transl
XX Pseudo
XX Pseudo
XX Pseudo
XX Pseudo
XX Pseudo
XX Pseudo
XX AT ANOV
XX ANOV
XX ANOV
XX O8-NOV
XX O8-NOV
XX O8-NOV
XX O8-NOV
XX O8-NOV
XX O8-NOV
XX OMERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 26 describes the construction of pvC-ompA-PEGAG.

The HIV GAG gene was obtained from plasmid HIVpBR322 by
CC Pick with oligonucleotide primers which added a SacII site
CC adjacent to the ATG codon of GAG to give the sequence of
CC AAQ38412, and a SacI site immediately after the termination
CC codon at the 3' end to give the sequence shown in AAQ38413.

CC rhe PCR fragment was digested with SacII and ligated to the
CC plasmid pvC45DP+T, which had been digested with EcoRI, the 5',
CC overhang filled in by Klenow fragment, and digested with SacII.
CC overhang filled in by Klenow fragment, and digested with SacII.
CC overhang filled was named pvC-ompA-PEGAG (AAQ38414) and was
CC verified by a partial sequence at the SacII junction. This
CC construction fuses the binding and translocation domains of PE
CC compA leader sequence. Alternatively, any vector contg. the complete
CC coding region for HIV-I GAG can be used with these oligomers to generate
CC the HIV GAG gene by HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                   QV
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 73-77; 85pp; English
                                                                                                                                                                       Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; matrix protein; Ma; Pseudomonas exotoxin; cell recognition translocation domain; anti-viral agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                 Pseudomonas exotoxin
                                                                                                                                                                                                                                                              25-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                                                                  AAR36807 standard; Protein; 414 AA.
                               08-NOV-1991;
                                                          04-NOV-1992;
                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130
                                                                                     12-MAY-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                              131
                                                                                                                                                                                                                                                                                                                                                                                         11
250 rv 251
                                                                                                                                                                                                                                                                                                                                                                                                                      251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHY
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                                                                                                                                                                                                                                                                                                                                                                                                                      RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   937 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                             aeruginosa
                                 91US-0792507
                                                            92EP-0310067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.2%;
95.5%;
                                                                                                                                                                                                                                 domains I and II encoded by pVC-PEBT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1207; DB 1
Pred. No. 5e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            937;
                                                                                                                                                                                             domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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(MERI ) MERCK

& CO INC

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RESULY 11
AAR324
XX AAR324
XX AAR324
AC AAR324
XX PE; Ps
KW T7 Poll
XX PE; Ps
KW T7 Poll
XX Synthe
XX EP532C
YN EP532C
XX Donnel
PI Montg:
XX WPI; DDR WPSD:
XX WPSD:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Donnelly JJ, F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful as
parasites
                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                        PE amino acids 2-414.
                                                                                                                                                                                                                                                                                    AAR32455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Control plasmid pVC-PEBT encodes a T7 promoter-driven gene sonsisting of PE amino acids 2-414 followed by termination instead of by at least part of the influenza A virus Matrix protein (as in e.g. AAQ41714).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 30-32; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                                                            02-SEP-1992;
                                                                                                                                                                                                                                            20-JUL-1993
                                                                                         09-SEP-1991;
            N-PSDB; AAQ37108
                    WPI; 1993-087107/11
                                                  Donnelly
                                       Montgomery DL,
                                                                    (MERI ) MERCK
                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                          polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1993-154266/19
DB; AAQ41715.
                                                                                                                                                                                                                                                                                                                                  PRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                        AEEAFDLWNECAKACYLDLKDGVRSSRMSVDPAIADTNGGGVLHYSMYLEGGNDALKLAI 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                       aeeafdlwnecakacvldlkdgvrssrmsvdpaiadtngggvlhysmvleggndalklai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                , נינ
                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedman A,
, Oliff AA,
                                       Friedman A,
    Oliff AI,
                                                                    & CO INC
                                                                                         91us-0756249
                                                                                                            92EP-0202660
                                                                                                                                                                                           fusion;
                                                                                                                                                                                       exotoxin; influenza A virus; M1; matrix protein;
fusion; hybrid; pvC-PEBT; pvC-PEM1-2.
                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.3%;
                                       Hawe LA,
Shi x, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hawe LA,
Shi x, t
                                                                                                                                                                                                                                                                                    414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1195; DB 14;
Pred. No. 2.7e-116;
                                                                                                                                                                                                                                                                                    ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                       Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ţ, Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                  Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                  SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion codons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
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                                                                                                                                                                                                                                                                                                                                                                                              205
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RESULT 1
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Query Match
Best Local S
Matches 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5 describes the construction of pVC-PEBT. A control plasmid was constructed which encodes a T7 polymerase driven gene fusion consisting of PE amino acids 2 to 414 followed termination codons. pVC-PEMI-2 was digested with SacII and EcoRI remove the M1 sequence. The vector was gel purified and ligated tan oligonucleotide that builds back PE codon no. 414 followed by termination signals shown in AAQ37893. The resulting construction was named pVC-PEBT (AAQ37108).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human
                                                                                                                                                                                                                       Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; matrix protein; Ma; Pseudomonas exotoxin; cell recognition translocation domain; anti-viral agent; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 33-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              papilloma:virus
                                                                                                                                                                                        Chimeric
                                                                                                                                                                                                  Chimeric Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                       AAR36806 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                      08-NOV-1991;
                                          04-NOV-1992;
                                                                                      EP541335-A.
                                                                                                                                 Region
                                                                                                                                                      Region
(MERI ) MERCK & CO INC
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                                                                                                                                                                                                                                                                    domains I and II fused to influenza A virus
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                                                                                                                                                                                                                                                                                                                                                                                            nagnqlshmspiytiemgdellaklardatffvrahesnemqptlaishagvsvvmaqtq
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          il Similarity
227; Conser
                                                                                                                                                                                        Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                           (first entry)
                      91US-0792507
                                           92EP-0310067
                                                                                                                                /note- "PE domains I
415..426
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.3%;
                                                                                                          "amino acids 57-68
Matrix protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85pp;
                                                                                                                                                                                                                                                                                                                                       426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1195; DB 14;
Pred. No. 2.7e-116;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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                                                                                                                                             and
                                                                                                                       of.
                                                                                                                       Influenza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 414;
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                                                                                                                       A Virus
                                                                                                                                                                                                                                     domain;
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PE;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matrix protein) was subcloned into BS-PE, a plasmid constructed by inserting a 1.3kb Nruf/SacII fragment of plasmid pVC45-DF+T containing the domain I and II coding regions of Pseudomonas exotoxin into pBluescript II SK restricted with HincII and SacII. The PE-derived portion of the hybrid protein allows internalisation of the protein by an antigen-presenting cell. The hybrid protein is then processed and an antigenic segment (i.e. the Influenza A virus matrix protein) is presented on the cell surface where it elicits an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An
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Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA encoding bacterial toxin-antigen conjugates useful as vaccines against viral infections, tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-154266/19
                                                                                                                                                                                                                                                                                                             PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; ompA; leader; signal; fusion; hybrid; BS-PEMa-1; pVC45DR+T; pVC-OmpA-PEMa-1; T7 promoter; RBS; ribosome binding site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR32454 standard;
  (MERI ) MERCK
                                                  09-SEP-1991;
                                                                                                 02-SEP-1992;
                                                                                                                                                 17-MAR-1993.
                                                                                                                                                                                              EP532090-A.
                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                            PE(2-414)-Ma(57-68) hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1993
                                                                                                                                                                                                                                                                                           initiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNALSITSDGLTIRLEGGVEPNKPVRYSYTROARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dnalsitsdgltirleggvepnkpvrysytrqargswslnwlvpighekpsnikvfihel 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fragment (encoding cein) was subcloned
                                                                                                                                                                                                                                                                                         sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.3%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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, Oliff AA,
                                                    91US-0756249
                                                                                                 92EP-0202660
       င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 426
       INC
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                                                                                                                                                                                                                                                                                           build-back
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Shi X, (
                                                                                                                                                                                                                                                                                                                                                                                                            protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1195; DB 14;
Pred. No. 2.8e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acids 57-68 of influenza A virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,:
                                                                                                                                                                                                                                                                                                                                           matrix protein;
pVC45DR+T;
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CC Example 4 describes the subcloning of PEMa from BS-PEMa-1 into CC BVC45DF+T. The PEMa insert (AAQ37890) was prepd. by restricting CC BS-PEMA-1 with SacI and removing the 3' overhang by treatment with CC BS-PEMA-1 with SacI and removing with ApaI and gel purifying. CC pVC45DF+T was restricted with EcoRI and the 5' overhang filled in CC with Klenow enzyme treatment. It was subsequently restricted with CC ApaI and gel purified. The vector and fragment were ligated together, CC and the resulting construction was named pVC-ompA-PEMa-1. CC The ompA signal sequence was removed from pVC-ompA-PEMa-1 by CC digestion with XbaI and HindIII. An oligonucleotide fragment contg. The Try promoter, ribosome binding site, initiation sequence and a build-back of the 5' end of the PE coding region (AAQ37891) was CC build-back of the vector. The resulting plasmid construct was named CC pVC-PEMa-1 and encodes a T7 polymerase-dilven gene fusion consisting CC of PE amino acids 2 through 414 joined to influenza Ml amino acids CC T to 68 (Ma) (AAQ37892).
                                                                                                                                                                                                            RESULT 1
AAR40102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
FHXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 227; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-lymphocyte immune infections, e.g. by papilloma:virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 30-31; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Montgomery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Donnelly JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                    steric
                                                              target site; cytotoxin; unpaired cysteine; monoclonal antibody; ligand; cell surface;
                                                                                                                   Pseudomonas exotoxin for site-specific mutation with unpaired
                                                                                                                                               27-JAN-1994
                                                                                                                                                                                                    AAR40102 standard; Protein;
                         Pseudomonas
                                                                                          Pseudomonas exotoxin; PE; diphtheria toxin;
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                                                                                                                                                                                                                                                                 NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ
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                                                    unpaired
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                          aeruginosa
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, Oliff AI,
                                                                                                                                                (first entry)
                                                    cysteine;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           influenza virus, HIV and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hawe
Shi x
                                                     s.u.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1195; DB 14;
Pred. No. 2.8e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ulmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J;
                                                                    receptor; binding
mutation;
                                                                                               DT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marshall MS;
                                                                                               immunotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                   site
                                                                                                                           CYS.
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                                                                                                                                                                                                                                                                                                              or near the cytotoxin's receptor-binding site, and retains the same receptor-binding ability and cytotoxicity as the native cytotoxins provided they are not conjugated with a binding mol. The toxins are cross-linked through the free SH group of their unpaired cysteine residues to binding mols. (including monoclonal antibodies, fragments and other ligands) to form immunotoxins, and these immunotoxins do not bind to the cell surface receptors which are bound by the native cytotoxin. However, when the cross-linker is cleaved and the binding mol. is released, the cytotoxin regains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site-specifically mutated cytotoxin(s) with an unpaired cysteine - such that conjugation of a binding mol. to the Cys blocks receptor binding used as immuno:toxins for highly specific
                                                                                                                                                                                                                                                                     Sequence
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   121
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                                                                                                                                                                                                                                                                                                  receptor-binding ability and its cytotoxicity.
NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 205
                                                                                                                                         AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGGGVLHYSMVLEGGNDALKLAI 85
                                                              {\tt aeeafdlwnecakacvldlkdgvrssrmsvdpaladtngqgvlhysmvleggndalklain}
                                                                                           DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
                                                                                                                                                                                                                                                                   613 AA;
                                                                                                                                                                                        Conservative
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182
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192
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188
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158
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245
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223
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Pred. No. 4.8e-116;
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                                                                                                                                                                                                                                                                                                                                                                    Site-specifically mutated cytotoxin(s) with an unpaired cysteine - such that conjugation of a binding mol. to the Cys blocks receptor binding used as immuno:toxins for highly specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  target site; cytotoxin; unpaired cysteine; monoclonal antibody; ligand; cell surface; steric unpaired cysteine; s.u.c.
                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                         The new mutated toxin has an unpaired cysteine residue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9315113-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-1994
                                                                                                                                                                                                           are bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TANO-) TANOX
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                                                                                                                                                                              e bound by the native cytotoxin. However, when the cross-linker cleaved and the binding mol. is released, the cytotoxin regains receptor-binding ability and its cytotoxicity.
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           DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
dnalsitsdgltirleggvepnkpvrysytrqargswslnwlvpighekpsnikvfihel
                                                                                               Similarity 100
27; Conservative
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                                                                                                                                                                                                                                                                                                                                 Page 20-23; 30pp; English.
                                                                                                                                                          613
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                                                                                                           Score 1195; DB 14;
Pred. No. 4.8e-116;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2

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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                           DB
                     US-08-225-224-1
US-08-255-224-1
US-09-046-992-2
US-08-665-259-25
US-08-762-500-75
US-08-762-500-75
US-08-846-340-4
US-08-846-340-4
US-08-846-340-3
US-08-846-340-3
US-08-846-340-3
US-08-846-340-3
US-08-846-340-3
US-08-846-348-26
US-08-845-65800-3
US-08-457-65800-3
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US-08-405-615-1
US-08-461-234-1
US-08-463-480-1
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9 Appl
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                                                Query Match
Best Local Similarity
Matches 252; Conserv
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	82
73.5	73.5	73.5	73.5	73.5	74	74	74	74	74.5	74.5	74.5	74.5	74.5	76	76	76.5	76.5
5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.7	5.8	5.8
352	224	224	224	224	435	435	337	337	2647	2647	551	551	550	1794	1489	599	349
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US-07-923-260A-6	PCT-US94-14498A-2	US-08-849-764C-2	US-09-111-070-2	US-08-588-163-2	US-09-066-047-13	US-09-066-046-27	US-08-871-572B-4	US-08-871-572B-1	US-08-779-113-8	US-08-583-562B-8	US-08-417-210A-143	US-08-417-210A-137	US-08-417-210A-140	5183745-6	5183745-2	US-09-000-145-2	US-08-970-428A-14
Sequence 6, App.	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 13, App	Sequence 27, App	Sequence 4, Appl.	Sequence 1, Appl	Sequence 8, Appl	Sequence 8, Appli	Sequence 143, App	Sequence 137, App	Sequence 140, App	Patent No. 518374	Patent No. 518374	Sequence 2, Appl	Sequence 14, App

ALIGNMENTS

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RESULT 1
US-09-047-148-2
; Sequence 2, Application US/09047148
; Patent No. 6086900
; GENERAL INFORMATION:
US-09-047-148-2
                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,148
FILING DATE: CONCURRENTLY Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,056
FILING DATE: 26-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: UTSE:072
REFERENCE/DOCKET NUMBER: UTSE:072
TELECOMMUNICATION INFORMATION:
TELECHANCE: (512) 418-3000
TELECHANCE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Draper, Rockford
TITLE OF INVENTION: METHODS AND COMPO:
TITLE OF INVENTION: CELL MEMBRANE-PENETRAT
TITLE OF INVENTION: CELL MEMBRANES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATTOIC, White & Durkee
STREET: P.O. Box 4433
                                                                                                         TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: F. CITY: Houston
STATE: Texas
COUNTRY: Unite
7TP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                           TYPE: amino acid STRANDEDNESS:
                     TOPOLOGY:
                                                                                    LENGTH:
                                                                                         638 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States
                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHODS AND COMPOSITIONS FOR USING MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS CELL MEMBRANES
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1 MHLIPHWIPLVASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA 60

Conservative

100.0%; J.08; 0;

Score 1323; DB 3; Pred. No. 3e-137; Mismatches 0;

Indels Length

Gaps

0;

638; 0;

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US-08-405-615-1
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                                                   Matches 227;
                                                                  Best Local Similarity
                                                                             Query Match
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with TITLE OF INVENTION: Increased Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pastan, ira APPLICANT: FitzGerald, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Sa
STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \vdash
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                               TOPOLOGY: li
                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                      LENGTH:
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08405615
                                                                                                                                TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Ellen L. Weber One Market Plaza, Steuart Tower, Suite
                                                                                                                                                                                     613 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                             415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version
                                                    Conservative
                                                                                                                                              ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252
                                                                 90.3%;
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                                                                                                                                                                                                                                                                    15280-36
                                                     0;
                                                     Score 1195; DB 1;
Pred. No. 3.8e-123;
0; Mismatches 0;
                                                                              Length 613;
                                                        Indels
                                                        0,
                                                        Gaps
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US-08-461-234-1
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                                                                                              Query Match
Best Local :
                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 TELEFAX: (415) 543-50 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 05-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                       APPLICATION 15-MAR INFORMEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
Weber, Ellen Lauver
32,7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                   MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                      NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US UFFILING DATE: 18-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                              Local Similarity es 227; Conserv
                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                     26
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                           AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAI 60
DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
                                          AEEAFDLWNECAKACYLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMYLEGGNDALKLAI 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94105-1492
                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                           (415)
                                                                                90.3%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pastan,
                                                                                                                                                                . protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                           (415)
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15-MAR-1995
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                                                                                                                                                                                                                                                                                543-5043
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                                                                                                                                                                                                                                                                                              543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increased Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant Pseudomonas Exotoxin with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08461234
                                                                                                                                                                                                                                                                                                                                                                                                                                 US 07/901,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/461,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            David J.
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                                                                                    0;
                                                                                                 Score 1195; DB 2; pred. No. 3.8e-123;
                                                                                                                                                                                                                                                                                                                          15280-36-3
                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #1.30
                                                                                       0,
                                                                                                                Length 613;
                                                                                       Indels
                                                                                       0;
                                                                                       Gaps
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RESULT 4
US-08-463-480-1
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ETLING DATE: 15-MAR-1995
ATTORNEY_AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE_DOCKET NUMBER: 15280-36-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08463480 Patent No. 5854044
                                                                                                                                                          Query Match 90.3%; Score 1195; DB 2; Length 613; Best Local Similarity 100.0%; Pred. No. 3.8e-123; Matches 227; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pastan, Ira H. APPLICANT: FitzGerald, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,709
EILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                TOPOLOGY: 15
                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 PRREKRWSEWASGKVLCLLDPLDGVYNYLAQORCNLDDTWEGKIYRV 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/463,480 FILING DATE: 05-JUN-1995 CLASSIFICATION: 435
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CITY: San Francisco
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DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
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                                                                                 AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAI 60
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OTHER INFORMATION: /label- native-PE
US-08-225-224-1
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NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 227; Conserv
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APPLICANT: PASTAN, Ira
APPLICANT: KREITMAN, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8-APR-1994
CIACCIPETATION.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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146 NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 205
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                                                                             DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
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                                                                                                                                                                                                 Query Match
Best Local :
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-APR-1995
PRIOR APPLICATION UDATA:
APPLICATION UNBER: US 08/225,224
FILING DATE: 08-APR-1994
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APPLICATION NUMBER: WO PRILING DATE: 06-APR-1995
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NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,7
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     146
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OPERATING SYSTEM:
SOFTWARE: PatentJ
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CITY: San Francisco
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                            26 ABEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGGGVLHYSMVLEGGNDALKLAI 85
                                                                                                                                                                              Local Similarity 100.
les 227; Conservative
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                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein LOCATION: 1..614
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 NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 205
                                                                                                        AEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAI 61
                                     DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 121
                                                       DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
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Two Embarcadero Center, Eighth Floor
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Puri, Raj K.
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08-JAN-1997
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                                                                                                                                                                                                                                                                                                         /note= "native Pseudomonas exotoxin
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Pred. No. 3.8e-123;
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PCT-US95-04468-1
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; OTHER INFORMATION:
PCT-US95-04468-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 614 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08, FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,7(
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-APR-CLASSIFICATION:
PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 PRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRV
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OPERATING SYSTEM: PC-DOS/MS-DOS
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les 227; Conserv
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                                                            NAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 181
                                                                          NAGNOLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQTQ 205
                                                                                                                      DNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 121
                                                                                                                                       DNALSTTSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL 145
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100.0%; Pred. No. 3.8e-12
ative 0; Mismatches 0
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US-09-046-992-2; Sequence 2, Application US/09046992

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                              US-08-665-259-25

; Sequence 25, Application US/08665259

; Patent No. 6028173
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; FRAGMENT TYPE:
US-09-046-992-2
                                                                                        RESULT
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NAME: POISSANT, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 9457
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lorberboum-Galski, Haya
APPLICANT: Yarkoni, Shai
APPLICANT: Yarkoni, Shai
TITLE OF INVENTION: METHODS OF CANCER DIAGNOSIS
TITLE OF INVENTION: USING A CHIMERIC TOXIN
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
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APPLICANT:
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CITY: New York
STATE: NY
                                                                                                                                         199 VVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGKIYRV 252
                                                                                                                                                                                                                 136 KVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVS
                                                                                                                                                                                                                                                   139 KVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVS 198
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                                                                                                                                                                                                                                                                                                                                                                               19 GGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGOGVLHYSMVLEGGN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 635 amino acids
                                                                                                                                                                                                                                                                                                         DALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNI 138
                                                                                                                                                                                                                                                                                    DALELAIDNALSITSDGLTIRLEGGVEPNKPLRYSYTRQARGRWSLNWLVPIGHEKPSNI 135
                                                                                                                                                                                                                                                                                                                                                            GGSGGGGGGGQAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                     223;
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1155 Avenue of the Americas
Landes, Gregory M.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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95.3%;
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Pred. No. 1.4e-121;
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RESULT 10
US-08-762-500-25
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Best Local
                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT:
                             APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING,
NUMBER OF SEQUENCES: 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LENGTH: 1684 amino acids
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                   CORRESPONDENCE ADDRESS:
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STATE: Macco
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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ADDRESSEE:
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Van Raay, Terence J.
Klinger, Katherine W.
KVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
VENTION: COMPOSITIONS, METHODS OF MAKING,
EQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burn, Timothy C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENZYME CORPORATION
GENZYME CORPORATION
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22.9%;
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STREET: One Mount CITY: Framingham

One Mountain Road

Massachusetts

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Best Local Similarity
                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                        Sequence 75,
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/I
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/762,500
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                    APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: COMPOSITIONS, METHODS OF M
NUMBER OF SEQUENCES: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 YTRQARGSWSLNWLVPIGHEKPSNIKVFIH-----ELNAGNQLSHMSPIYTIEMGDE 165
                                                                                                                                                                                                                                                                                                                                                                                               836 ALQYQHERRASDWAVDSNLCGAMDPSDGIGALIEEER 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 LLAKLARDATFFVRAHESNEMQPTLAISHAGVSVV------
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 01701
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                                   STREET: One Mount
CITY: Framingham
                                                                ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                       5, Application US/08762500 6030806
               Massachusetts
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                                                   One Mountain Road
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                                                                                                                                                                                                                                    Burn,
                                                                                                                                                                                                                                                     Landes,
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                Timothy
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States of America
                                                                                                                                                                                                                                        Gregory M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 93.5; DB 3; Length 1684; 22.9%; Pred. No. 0.59;
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                                                                                                                          HROMOSOME 16 GENES,
METHODS OF MAKING AND USING
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; MOLECULE TYPE: protein US-08-762-500-75
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Best Local Similarity 22.9%;
Matches 36; Conservative 2
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APPLICANT: Collins
APPLICANT: Donalds
APPLICANT: Fitz, LA
APPLICANT: Neben,
                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, April 19 No. 57
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INFORMATION FOR SEQ ID NO: 75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: PCT/US96/10469
APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/665,259
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                   APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
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OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM:
                                                                       ZIP: 02140
                                                                                                                             Cambridge
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)GY: linear
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IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                      Floppy disk
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-609-572-4
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Brown, Scott A.
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                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRECTOR:
                               ATTORNEY/AGENT INFORMATION:
                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 32,724
                                                   FILING DATE:
                                                                                                 CLASSIFICATION:
                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                     APPLICATION NUMBER:
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Neben, Tam
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Pred. No. 0.23;
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; MOLECULE TYPE: protein US-08-841-751-4
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Best Local Similarity
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              TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
                                                                          REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GITTELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
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APPLICATION NUMBER:
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CITY: Cambridge
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ZIP: 02140
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STREET: 87 CambridgePark Drive
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LENGTH:
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380 amino acids
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Fitz, Lori
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(617) 876-5851
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20.7%; Pred. No. 0.
                                                                                                                                                                                                                     08/609,572
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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-846-340-4
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US-08-846-344-4
                                                                                             ; MOLECULE TYPE: protein US-08-846-344-4
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Best Local Similarity
Matches 34; Conserv
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Query Match
Best Local Similarity 20.7
Matches 34; Conservative
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APPLICANT: Collin:
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APPLICATION NUMBER: 08/609,57
APPLICATION NUMBER: 08/609,57
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 498-8224
                                                                                                                                                               TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
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APPLICANT: Wood, Clive
TITLE OF INVENTION: CYT
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                   6.7%; Score 88; DB 4; Length 380; 20.7%; Pred. No. 0.23;
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Search completed: November 13, 2001, 14:26:52 Job time: 38 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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exotoxin A precursor PAll48 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa (C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000 C;Accession: C83503 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,

RESULT C83503

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HESNEMQPTLAISHAGVSVVMAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN

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DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG

В

RESULT 1 A30347 A30347 A30347 exotoxin A precursor - Pseudomonas aerugi C; Species: Pseudomonas aeruginosa C; Date: 08-Jun-1990 #sequence_revision 08 C; Accession: A30347 R; Gray, G.L.; Smith, D.H.; Baldridge, J.S Proc. Natl. Acad. Sci. U.S.A. 81, 2645-26 A; Title: Cloning, nucleotide sequence, an A; Reference number: A30347; MUID:84194063 A; Accession: A30347 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-638 <gra> A; Cross references: GB:K01397; GB:M23348; C; Superfamily: Pseudomonas aeruginosa exo C; Keywords: exotoxin  Query Match Best Local Similarity 100.0%; Score Best Local Similarity 100.0%; Pred Matches 252; Conservative 0; Mism</gra>	30 31 31 31 31 31 31 31 31 31 31 31 31 31
precursor - pseudomonas -Jun-190 #s -Jun-1	82.5 82.8 82.8 81.5 81.5 81.8 81.8 81.8 81.8 81.8 81
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<pre>ext_change 24-Nov-1999 R.N.; Vasil, M.L.; Chen, E.Y.; H in Escherichia coli of the exot in Escherichia coli of the exot ; PIDN:AAB59097.1; PID:g151216 ; Length 638; ; Indels 0; Gaps 0;</pre>	probable binding p thiamin-monophosph conserved hypothet integrin beta-4 ch citrate lyase, bet beta-lactamase (EC hypothetical prote anthranilate synth speract receptor p hypothetical prote hypothetical prote sodium channel alp sodium channel alp probable invasin 2 hypothetical prote hypothetical prote

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; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337
A;Accession: C83503
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C;Superfamily: Pseudo
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A;Experimental source: strain PAO1
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A; Residues: 1-638 <STO>
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R;Connors, T.D.; van Raay, T.J.; Petry, L.R.; Klinger, K.W.; Landes, G.M.; Burn, Genomics 39, 231-234, 1997
A;Title: The cloning of a human ABC gene (ABC3) mapping to chromosome 16p13.3.
A;Reference number: A59188; MUID:97179225
A;Accession: A59188
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A;Map position: 16p13.3-16p13.3
C;Superfamily: ATP-binding cassette homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000
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                                   166 LLAKLARDATFFVRAHESNEMQPTLAISHAGVSVV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHLIPHWIPLVASLGLLAGGSSASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTNGQGVLHYSNVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HESNEMOPTLAISHAGVSVVMAQTOPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHLTPHWIPLVASIGLLAGGSFASAAEEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA 60
                                                                  FLKQKYGAGYHMTLVKEPHCNPEDISQLVHHHVPNATLESSAGAELSFILPRESTHRFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDDTWEGKIYRV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                          Conservative
                                                                                                                                                        7.18; 22.98;
   EKKQKELGIASFGASITTMEEVFLRVGKLVDSSMDIQAIQLP
                                                                                                                                            22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 2.
                                                                                                                                                          Score 93.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
2.5e-107;
nes 3;
                                                                                                                                                                             DB 2;
                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 638;
                                                                                                                                                                             Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                             Indels
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                                        -MA 202
                                                                                                                                               Gaps
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                                                          RESULT
G83559
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C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1100-1120/Domain: transmembrane #status predicted <TM7>
F;1145-1169/Domain: transmembrane #status predicted <TM8>
F;1181-1207/Domain: transmembrane #status predicted <TM9>
F;1181-1207/Domain: transmembrane #status predicted <TM1>
F;1215-1236/Domain: transmembrane #status predicted <TM11>
F;1245-1264/Domain: transmembrane #status predicted <TM11>
F;1299-1324/Domain: transmembrane #status predicted <TM12>
F;1399-1590/Domain: drp-binding cassette homology <ABC2>
F;1399-1590/Domain: drp-binding cassette homology <ABC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:ABC3
A;Cross-references: GDB:3770735; OMIM:601615
A;Cross-references: GDB:3770735; OMIM:601615
A;Map position: 16p13.3-16p13.3
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding C;Superfamily: unassigned ATP-binding cassette protein; phosphoprotein; C;Keywords: ATP binding; nucleotide binding; P-loop; phosphoprotein; C;Keywords: ATP binding; nucleotide binding; P-loop; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable ATP-binding cassette transporter ABC-3 - human N,Alternate names: ATP-binding cassette transporter ABC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RE;Klugbauer, N.; Hofmann, F.
FEBS Lett. 391, 61-65, 1996
A;Title: Primary structure of a novel ABC
A;Reference number: S71363; MUID:96326608
                                                                                                                                                                                                              F;1346-1423/Region: nucleotide-binding motif A (P-loop)
F;1535-1540/Region: nucleotide-binding motif B
F;674,866,1524/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent F;1344/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;549-739/Domain: ATP-binding cassette homolo F;566-573/Region: nucleotide-binding motif A F;685-690/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F; 373-394/Domain:
F; 401-422/Domain:
F; 452-475/Domain:
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F; 307-329/Domain:
F; 345-364/Domain:
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A; Residues: 1-1704 < KLU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 QTQPRREKRWSEWASGKVLC-LLDPLDGVYNYLAQQR 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n: transmembrane #status predicted <TM1>
n: transmembrane #status predicted <TM2>
n: transmembrane #status predicted <TM2>
n: transmembrane #status predicted <TM4>
n: transmembrane #status predicted <TM4>
n: transmembrane #status predicted <TM6>
n: transmembrane #status predicted <T
7.1%; 22.9%;
Score 93.5;
Pred. No. 12;
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                                                                  DB
                                                      2;
                                                            Length 1704;
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transmembrane
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brane pr
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hypothetical protein PA0690 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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Best Local :
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                                                                                                                                                                   856
                                                                                                                                                                                                          203 QTQPRREKRWSEWASGKVLC-LLDPLDGVYNYLAQQR 238
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                                                                                                                                                                                                                                                                                                                                                                                                 114 YTROARGSWSLNWLVPIGHEKPSNIKVFIH-----ELNAGNQLSHMSPIYTIEMGDE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 22.9 los 36; Conservative
                                                                                                                                                                 ALQYQHERRASDWAVDSNLCGAMDPSDGIGALIEEER
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                                                                                                                                                                                                                                                             -EKKQKELGIASFGASITTMEEVFLRVGKLVDSSMDIQAIQLP 855
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C:Species: phage SPP1
C:Date: 25-Dec-1994 #sequence_revision 26-May-1995 #text_change 17-Nov-2000
C:Date: 25-Dec-1999; T42331; S41173
C:Accession: S43799; T42331; S41173
R:Pedre, X: Weise, F: Chai, S: Lueder, G.; Alonso, J.C.
J. Mol. Biol. 236, 1324-1340, 1994
A:Title: Analysis of cis and trans acting elements required for the initiat: A:Reference number: S43798; MUID:94172631
A:Accession: S43799
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X67865; NID:g472886; PIDN:CAA48050.1; PID:g439630 A;NOte: the nucleotide sequence was submitted to the EMBL Data Library, July R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A. Gene 204, 201-212, 1997
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A;Residues: 1-4180 <STO>
A;Cross-references: GB:AE004504; GB:AE004091; NID:g9946568; PIDN:AAG04079.1;
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A;Accession: G83559
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                                                                                                                                                                                                                                                                                                                                                                          A; Title: The complete nucleotide sequence and functional organization A; Reference number: Z22137; MUID: 98094274 A; Accession: T42331
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A;Molecule type: DNA
A;Residues: 1-136,'Y',138-311 <ALO>
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R;Stover, C.K.; Pham, X.Q.;
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Best Local S
Matches 35
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Best Local S
Matches 50
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151
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mes 35; Conserv
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                                     RYSYTROARGSWSLNWLVPIGHEKPSNIKV-----FIHELNAGNOLSHMSPIYTIEMGD 164
                                                                                                                             RMSVDPAIAD-TNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPV 110
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                                                                                                                                                                         21;
                                                                                                                                                                       Score 90.5; DB pred. No. 2.1; Mismatches
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Pred. No. 4
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-NIKVVEADFAYVVALIGGNKYKH---
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Larbig, K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1992
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probable replication licensing factor MCM6 - Caenorhabditis elegans N;Alternate names: hypothetical protein ZK632.1 C;Species: Caenorhabditis elegans C;Date: 06-Jan-1995 #sequence_revision 19-Jul-1996 #text_change 24-S C;Accession: S40933 #Sequence_revision 19-Jul-1996 #text_change 24-S C;Accession: S40933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X64700; NID:g54807; PIDN:CAA45941.1; PID:g54808 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Fel C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin C;Keywords: muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S20900
R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick,
EMBO J. 11, 1711-1716, 1992
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C;Superfamily: cyclopropane-fatty-acyl-phospholipid C;Keywords: cell cycle control; DNA replication; me: F;1-365/Domain: MCM homology (fragment) <MCM>
                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z22181; NID:g297998; PID:g297999 C;Comment: The complex of six MCM proteins is one of seve
                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data A; Reference number: S40933
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A; Residues: 1-531 <LAB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                        A; Map position: 3
A; Introns: 463/2
                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-521 <BER>
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                                                                      A; Description: part of the replication licensing system that permits DNA replication
                                                                                                  C; Function:
                                                                                                                       C; Complex: The predominant form is a heterohexamer
                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                              A; Accession: S40933
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                                                                                                                                                                                                                       phosphorylated and dissociate from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 DPAIADTNGQGVLHYSMVLEGGN--DALK--LAIDNALSITSDGLTIRLEGGVEPNKPVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSKIIQYIVEMQAKNTDKWSECARVK-----SLDAVITNLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSVV----MAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAAIIDVTSS---FTSLVLDNVNRYDSGKYTLTLENSSGTKSAFVTVRVLD--TPSPPVN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELLAKLARDATFFVRAHESNEMOPTLAISHA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGCSYYFRVTAENEYGIGLAARTADPIKVAEVPQPPGKITVDDVTRNSVSLSWTKPEHDG
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                                                                                                                                                                                                                                                                                                                                                                                         Library, February 1993
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                           methyltransferase;
                                                                                                                       of MCM2,
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                                                                                                                       MCM4, MCM5,
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hypothetical protein SPAC8A4.09c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 31-Jan-2000 C;Accession: T39131; T41433; S62525 R;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γ
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A; Reference number: Z21993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-380 <SEE>
A;Residues: 1-380 <SEE>
A;Cross-references: EMBL:AL032824; PIDN:CAB37424.1; GSPDB:GN00068; SPDB:SPCC584.11c
A;Experimental source: strain 972h-; cosmid c584
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local S
Matches 55
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Best Local :
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                                                                                            368
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                                                                                                                                                                                                                                                                                                                                  Local Similarity
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   rabbit (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDAT 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SGKASSAAGLTAAVVKDEES----FEFVIEAGALMLADNGVCCIDEFDKM------DLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VL---LMLLGG--VAKKSRDEGTSLRGD-INVCLVGDPSTAKSQVLKAVEEFSP-RAIYT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEG------
                                                                                                                                                                                                    ---LNWLVPIGH------EKPSNIKVFIHELNAGNQL--SHMSPI-YTIEMGDELL- 167
                                                                                                                                                                                                                                       STIVNIGGIAMK----DKIISATVDNTIEHVETTLDPDTEWHEPTRISYEWDGKDAETYTE
                                                                                                                                                              DIHLSVDAPLGRRLQRIDVLAEIPSWLKGFVHGVSGTKPFIYQYFSPVKFTLKMGDEVIE
                                                                                            DEATLFNETTF 378
                                                                                                                             --AKLARDATF 176
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55; Conser
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                                                                                                                                                                                                                                                                                                                                    Score 89; DB Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                                       Length 380
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R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J. EMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C;Accession: S20901; 146520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 4235-5250 <LA2>
A;Cross-references: EMBL:X17329; NID:g1756; PIDN:CAA35207.1; PID:g930251
A;Cross-references: EMBL:X17329; NID:g1756; PIDN:CAA35207.1; PID:g930251
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;
C;Keywords: muscle
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A; Cross-references: EMBL: X64696
A; Cross-references: EMBL: X64696
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R; Labeit, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U
R; Labeit, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U
Rature 345, 273-276, 1990
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A;Accession: I46520
A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                   A; Cross-references: EMBL:X90568; NID:g1017424; PID:g1017425
R; Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Blochemistry 34, 553-561, 1995
A; Title: Dissecting titin into its structural motifs: idential procession: 138345; MUID:95119041
A; Accession: 138345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C;Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393
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                                A; Molecule type: mRNA
A; Residues: 1977-2014 <MUS>
                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-26926 <LAB1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Labeit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    titin, cardiac muscle [validated] - human
A;Cross-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1;
                                                                                            A;Status: nucleic
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4847 DAAIIDSTSS---FTSLVLDNVNRYDSGKYTLTLENSSGTKSAFVTVRVLD--TPSPPVN 4901
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                                                                                                acid sequence not
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22.1%;
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Pred. No. 1.9e+02;
Pred. Thes 79;
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                   PID:g602580
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submitted to the Brookhaven Protein Data Bank, August 1996 A;Reference number: A66201; PDB:INCT A;Contents: annotation; conformation by (1)H-NMR, residues
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A; Residues: 26831-26926 <GAU>
R; Improta, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A; Reference number: A66736; PDB:1TIT
A; Contents: annotation; conformation by (1) H-NMR, residues 52
B: Deferit
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A; Cross references: EMBL: X92412; NID:g1236761
R; Gautel, M.; Leonard, K.; Labeit, S.
EMBO J. 12, 3827-3834, 1993
A; Title: Phosphory Lation of KSP motifs in the A; Reference number: S37393; MUID:94008990
A; Accession: S37393
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A:Accession: S63665
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A; Residues: 'P',2278-22431,'R',22433-22448,'G',22450-22453,'Q',22455-22480,'TR'
A; Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
R; Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
J. Mol. Biol. 256, 556-563, 1996
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A;ResIdues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3>
A;Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1;
A;Accession: S20899
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A:Molecule type: mRNA
A:Residues: 13597-14200,'I',14202-14696 <LAB2>
A:Residues: 13597-14200,'I',14202-14696 <LAB2>
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Best Local Similarity
Matches 46; Conserv
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J. 11, 1711-1716, 1992
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                                                       YSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLA 171
                                                                                                              DAAIIDVTSS---FTSLVLDNVNRYDSGKYTLTLENSSGTKSAFVTVRVLD--TPSPPVN 16542
                                                                                                                                                                  DPAIADTNGQGVLHYSMVLEGGN--DALK--LAIDNALSITSDGLTIRLEGGVEPNKPVR 111
  LKVTEITKDSVSITWEPPL-LDGGSKIKNYIVEKREATRKSYAAVVTNCHKNSWKIDQLQ 16601
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                    6.7%; Score 89; 1
22.1%; Pred. No. 1
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                          Insect Biochem. Mol. Biol. 27, 133-147, 1997 A;Title: Biochemical, molecular, and phylogenetic A;Reference number: Z22655; MUID:97218699 A;Accession: T43735
A; Status: preliminary; translated from GB/EMBL/DDBJ
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hypothetical protein F20D1.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc C;Accession: T21147 R;Burton, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, August 1996
A;Reference number: Z19382
A;Accession: T21147
A;Status: preliminary; translated from GB/EMBL/DBJ
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                                    pyruvate carboxylase (EC 6.4.1.1) [validated] - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Au
                                                                                              RESULT
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A;Introns: 45/3; 75/3; 126/3; 166/2; 196/3; 243/3; 271/2; 321/1;
C;Superfamily: Caenorhabditis elegans hypothetical protein F20D1.
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C; Accession: T43735
R; Tu, Z.; Hagedorn, H.H.
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A; Residues: 1-915 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: F20D1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z78542; PIDN:CAB01748.1; GSPDB:GN00028; CESP:F20D1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16662 GSKIIQYIVEMQAKHSEKWSECARVKSL 16689
                                                                                                                                                                                                                                                       462
                                                                                                                                                                                                                                                                                                                               402
                                                                                                                                                                                                                                                                                                                                                                                                            359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172
                                                                                                                                                                            517
                                                                                                                                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 HVVPLKQSKYFRNHTVETFGLLATGPTSSLPFDILEIAATWRFFRENSLTENHSHSDFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y
y
                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 HWIPL------AEEAFDL
                                                                                                                                                                                                                                                                                                                                                                   KPSNIKVFIHELN----AGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEM 186
                                                                                                                                                                          LQCS
                                                                                                                                                                                                               QRCN 240
                                                                                                                                                                                                                                                       STVTWRLAIALANARVFMSD-QPRAEPQLWVEF----LLKLREKYEKMETVEKVYNGIDH 516
                                                                                                                                                                                                                                                                                                                             AESDNESLAHELNMLNAASMSENQLSDDELVNNVKLDTLFNYKNPKSANTFLAPYKCAKK 461
                                                                                                                                                                                                                                                                                                                                                                                                            OKLTINSASEVKIGKHAETEDSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                            LKLAIDNALSI-----TSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYSSYWNIKMKSTKSSLLGVLDEILGVYREDTRKAIRSDLNCALILGKHYTQ-KELPNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----WN---ECAKACVLDLKDGVRS-SRMSVDPAI-ADTNGQGVL--HYSMVLEGGNDA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSVV---MAQTOPRREKRWSEWASGKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGCSYYFRYTAENEYGIGLPAQTADPIKVAEVPQPPGKITVDDVTRNSVSLSWTKPEHDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDATFFVRAHESNEM----
                                                                                                                                                                                                                                                                                       QPT----LAISHAGVSVVMAQTQPRREKR-WSEWASGKVLCL-----LDPLDGVYNYLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.7%;
22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---QP---
                                                                                                                                                                                                                                                                                                                                                                                                            -NGPMPPALMK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96;
                                      #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TLAIS-----HAG
                                                                                                                                                                                                                                                                                                                                                                                                          SWVNFIFNE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388/3; 508/2; 552/1
.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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analysis

of.

pyruvate carboxylase

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A; Molecule type: mRNA
A; Residues: 1-1195 <TUZ>
A; Cross-references: EMBL:L36530; PIDN:AAB64306.1
A; Cross-references: EMBL:L36530; PIDN:AAB64306.1
C; Function: EC 6.4.1.1 [validated; MUID:97218699]
A; Description: EC 6.4.1.1 [validated; MUID:97218699]
C; Superfamily: pyruvate carboxylase; biotin carboxylase homolog
C; Keywords: ligase
C; Keywords: ligase
F; 1161/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 1
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1064 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: F86182
                                        QΥ
                                                                                                  В
                                                                                                                                                   Ωy
                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005172; NID:g7211974; PIDN:AAF40445.1; GSPDB:GN00141
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697 LNYLPNLI-----LGMEAAGNAGGVVEAAISYTGDVSDPTKKKYDLKYYTNLADELVKAG 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    752 THILCIKDMAGLLKPQAAKLLIAAIREKHPDVPIHTHTHDTSGAGVASMLACAEAGADVV 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 6.7%; Score 88; DB Local Similarity 21.6%; Pred. No. 22; es 50; Conservative 34; Mismatches
                                                                                                                                                                                                          601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                     661 LFSWPEHCRTYLTRIAAC-----RMRHPQWQTD---ADEVAAQDDEFSL-----NDSLK 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MHLIPHWIPLVASLGLLAGGSSASAAEEAF---
                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTMKSGNADVYLNEIPGGQYTNLQFQAYSLGLGDFFEDVKKAYREANLLL 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVAVDSMSGMTSQPSMGAVVASLQGTPLDTGLNLRDISEYSAYWEQTRTLYA-----PFE 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLAIDNALSITSD---GLTIR-----LEGGVEPNKPVRYS-YTRQARGSWSLNWLVPI- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----CVLDLKD------GVRSSRMSVDPAI--ADTNGQGVLHYSMVLEGGNDAL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGD--ELLAKLARDATFFV
                                              LAIDNALSITSDGLTIRLEGGVEPNK--PVRYSYTRQARGSWSLNWLVPIGHEKPSNIKV 140
                                                                                                                                                                                                       HGLPMVATKNGGPVDIHRALHNGLLVDPHDQEAIANALLKLVSEKNLWHECRINGWKNIH
                                                                                                                                                                                                                                                           HWIPLVASL------
  DVQDMSLRLSMDGDKPSLNGSLEPNSADPVKQIMSRMR--
                                                                                                                                                                                                                                                                                                               . Similarity 21.1 60; Conservative
                                                                                                                                                      -AKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALK 82
                                                                                                                                                                                                                                                                                                                                       6.6%;
                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                              -GLLAGGSSASAAEEAF-----DLWNEC-----
                                                                                                                                                                                                                                                                                                                                          Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biotin carboxylase homology; lipoyl/biotin-binding
                                                                                                                                                                                                                                                                                                                  Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
22;
                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1064; 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DLWNECAKA- 39
                                                                                                                                                                                                                                                                                                                       Indels
          -TPEIKSKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       660
             752
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C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57335; S57333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: S57335; S57333
R;Jenny, A.; Keller, W.
Nucleic Acids Res. 23, 2629-2635, 1995
Nucleic Acids Res. 23, 2629-2635, 1995
A;Title: Cloning of cDNAs encoding the 160
A;Reference number: S57333; MUID:95380277
A;Accession: S57335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-1444 <JEN>
A;Cross-references: EMBL:X83097; NID:g953171; PIDN:CAA58152.1; PID:g929007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cleavage and polyadenylation specificity factor 160K chain -
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                                                                                                               Qy
                                                                                                                                                       Вр
                                                                                                                                                                                        QΥ
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                                                                                                                                                                                                                                                                                                              DЪ
                                                                                                                                                                                                                                                                                                                                                 QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 188-197;204-216;403-423;426-437;511-519;573-580;780-789;1107-1116;1163-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S57333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
Вb
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       804 KAVRSDPQMAKN-----SGFAISTSMPLDELTRFLKSAKIQVSE 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 FIHELNAGNOLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVV
                                       206
                                                                              463
                                                                                                                   158
                                                                                                                                                         413
                                                                                                                                                                                          100 LEGGVE--PNKPVRYSYTROARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNOLSHMSPI 157
                                                                                                                                                                                                                                     358
                                                                                                                                                                                                                                                                                                              298 PYGVALNSLTTGTTAFPLRTQEGVRITLDCAQAAFISYDKMVISLKGGEIYVLTLITDGM 357
                                                                                                                                                                                                                                                                         49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                   9 PLVASLGLLAGGSSA--SAAEEAFDLWNECAKAC------VLDLK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MA-QTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ELQGKKQSDNLGSKYPVLRRERLVVLAVDCYDNEGAPDEKAMVPMIQ----
                                                                                                                                                                                                                                                                      RSSR-MSVDPAIADTNGQGVLHYSMV-LEGGNDALKLAIDNALSI----TSDGLTIR
PQ 524
                                                                            YSFEVCDSILNIGPCANAAMGEPAFLSEEFQNSPEPDLEIVVCSGYGKNGALSVLQKSIR 522
                                                                                                                 YTIEMGDELL----AKLARDATFFVRAHESNEMQPTLAI-----SHAGVSVVMAQTQ 205
                                                                                                                                                         EAADKEEPPSKKKRVDATT----GWSGSKSVP--QDEVDEIEVYGSEAQSGTQLA----T
                                                                                                                                                                                                                                 RSVRAFHFDKAAA-----SVLTTSMVTMEPGYLFLGSRLGNSLLLKYTEKLQEPPASTAR 412
                                       PR 207
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               6.6%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 87; DB 2; Length 1444; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine
                                                                                                                                                                                                                                                                                                                                                                                                     58;
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cleavage
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                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                 462
                                                                                                                                                                                                                                                                                                                                                                                                       13;
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po1

Search completed: November 13, Job time: 131 sec 2001, 14:28:25 THIS PAGE BLANK (USPTO)

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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"Crystal structure of the catalytic domain of Pseudomonas exotoxin complexed with a nicotinamide adenine dinucleotide analog: implications for the activation process and for ADP ribosylation."; proc. Natl. Acad. Sci. U.S.A. 93:6902-6906(1996).
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                                                                                                                                                                                                                                                                            Local Similarity
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1DMA; 15-SEP-95.
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                   SWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRA
                                                                                 DTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG
                                                                                                     DTNGGGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARG 120
                                                                                                                                                                   MHLIPHWIPLYASLGLLAGGSSASAAEBAFDLWNECAKACVLDLKDGVRSSRMSVDPAIA 60
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Signal;
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e of Pseudomonas aeruginosa exotoxin domain III
AMP: conformational differences with the intac
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98.8%;
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T -> I (IN REF. 1)
F -> S (IN REF. 1)
F -> S (IN REF. 1)
S -> T (IN REF. 1)
S -> V (IN REF. 1)
I -> V (IN REF. 1)
I -> V (IN REF. 1)
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                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IA (REQUIRED FOR RECOGNITION).
II (REQUIRED FOR
                                                                                                                                                                                                                                                                          Score 1307;
Pred. No. 5.
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V S (IN REF. 1).
V N (IN REF. 1).
V U (IN REF. 1).
V U (IN REF. 1).
V S (IN REF. 1).
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                                                                                                                                                                                                                                                                               .8e-108;
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RESULT 2
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30-MAY-2000
ATP-BINDING
TRANSPORTER
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Q99758; Q97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                           CHEMOTHERAPEUTICS DRUGS.

TISSUE SPECIFICITY HIGHLY EXPRESSED IN LUNG, FOLLOWED BY BRAIN,
PANCERAS, SKELETAL MUSCLE AND HEART. WEAKLY EXPRESSED IN PLACENTA,
KIDNEY AND LIVER. ALSO EXPRESSED IN MEDULLARY THYROID CARCINOMA
CELLS (MTC) AND IN C-CELL CARCINOMA.
CELLS (MTC) AND IN C-CELL CARCINOMA.
DOMAIN, MULTIFUNCTIONAL POLYPETIDE WITH TWO HOMOLOGOUS HALVES,
DOMAIN, MULTIFUNCTIONAL POLYPETIDE WITH TWO HOMOLOGOUS HALVES,
EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
APP BINDING CASSETTE (ABC) DOMAIN (BY SIMILARITY)
PRICHARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                       Genomics 39:231-234(1997).
-i- FUNCTION: MAY BE A TRANSPORTER,
FOUND YET (BY SIMILARITY). MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS
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                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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                                                                Pfam; PFO PROSITE;
                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                   "The cloning of a human ABC
16n13.3 ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96326608; PubMed-8706931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LDDTWEGKIYRV
                                                                                                        EMBL; X97187
MIM; 601615;
                                                                                                                   EMBL; U78735; AAC50967.1; -. EMBL; X97187; CAA65825.1; -.
                                                                                                                                                                                                                          between
                                                                                          InterPro; IPR001617;
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               TRANSMEM
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                                      TRANSMEM
                                                     ATP-binding;
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                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                               PF00005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q92473;
                                                                 00005; ABC_tran; 2.
PS00211; ABC_TRANSPORTER;
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(Rel. 39, Last annotation update)
CASSETTE, SUB-FAMILY A, MEMBER 3 (ATP-BINDING CASSETTE
3) (ATP-BINDING CASSETTE 3) (ABC-C TRANSPORTER).
7; Transport;
22 42
249 269
307 327
344 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39, Created)
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                            ; Transmembrane.
POTENTIAL.
POTENTIAL.
                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                                                                             gene (ABC3) mapping
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     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                           , ITS NATURAL SUBSTRATE HAS ACT AS AN EFFLUX PUMP FOR
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Best Local Similarity
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Ropora A., Sonnhammer D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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NP_BIND
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda;
                                                                     -!- SIMILARITY: BELONGS TO THE MCM FAMILY.
                                                                                              Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239
                                                                                                                                                                                                                                                                                                                         Rhabditidae;
                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
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                                                                                                                   .2 Mb of contiguous nucleotide sequence
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                                                                                                                                                                                                                                                                                                                       Peloderinae;
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                                                                               LOCATION: NUCLEAR
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22.9%;
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POTENTIAL.

ATP (POTENTIAL).
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-> S (IN REF. 2).
-> P (IN REF. 2).
AF0098DAF7A04F5F (
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No. 3
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RESULT
YC9B_SC
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Best Local
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EMBL; 222181; CAA80357.1; 
EMBL; 222181; CAA80191.1; 
EMBL; 229095; CAA80191.1; 
EMBC; 280905; CAA80191.1; 
WormPep; ZK632.1; CE00415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHPO
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SEQUENCE
                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungi; Ascomycota; Schizosacch
Schizosaccharomycetales; Schizosaccharomy
                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 43.0 KDA PROTEIN C584.11C IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00847; MCM_1; 1.

PROSITE; PS50051; MCM_2; 1.

Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; DNA replication; Cell cycle; ATP-binding.

DOMAIN 346 554 MCM.

NP_BIND 397 404 ATP (POTENTIAL).
                                                                                                                                                                                    Seeger K., Harris D., Wood V., Rajandream M.A., Barrell Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     Q09885;
01-FEB-1996
               Hypothetical
                                                                                                                                                                                                                                                                                                                                                       SPCC584.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     YC9B_SCHPO
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                                 EMBL; AL032824; CAB37424.1;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                        Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 LAGGSSASAAEEA--FDLWNECA---KACVLDLKDGVRSSRMSVDPAIADTNGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVGGDASGAVEETDYLDLWSKMSTEDRATLKKMSDDKKIEKNIVDSLFPNIYGNHEVKLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SGKASSAAGLTAAVVKDEES----FEFVIEAGALMLADNGVCCIDEFDKM------DLK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VL---LMLLGG--VAKKSRDEGTSLRGD-INVCLVGDPSTAKSQVLKAVEEFSP-RAIYT 420
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                                                                                                                                                                                                                                                                                                Ascomycota; Schizosaccnaromycetaceae; etales; Schizosaccharomycetaceae;
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91130 MW;
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   42961 MW;
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Pred. No. 3.3;
39; Mismatches
                                                                                                                                                                                                                                                                                                                  Schizosaccharomycetes;
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A65777B672310E68 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING PROTEIN).
IL13RA2 OR IL13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I132_HUMAN
                                                                                                                                                                       TISSUE=Renal cell carcinoma;
MEDLINE=96279273; PubMed=866
                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of a specific binding protein structurally related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                   Caput D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
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or send a
                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                        chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368
EMBL;
EMBL;
EMBL;
MIM;
                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                               MEDLINE-97321053;
Guo J., Apiou F.,
                                                                                                                                                                                                                                                                                                                   Donaldson
Henderson
                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                           use
                                                                                                                                                                                                                                  "Chromosome mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIHLSVDAPLGRRLQRIDVLAEIPSWLKGFVHGVSGTKPFIYQYFSPVKFTLKMGDEVIE
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                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
          X95302; CAA64617.1;
U70981; AAB17170.1;
Y08768; CAA70021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                        non-profit institutions as long as its content is in no way dand this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        D.D., Whitters M.J., Fitz L., Neben S.L., O'Hara R.M. Jr., Turner K.J., (OCT-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                       Laurent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176
                                                                                                                                                                                                                                                 Mellerin M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       P.,
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                                                                                                                                                                                                                                                              PubMed=9177784;
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Primates;
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26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380
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                                                                                               There are no rest
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IL-5 receptor alpha
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                                                                                                                                                                                                         INTERLEUKIN-13
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                                                                                                                                     a collaboration
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                                                                                      in no way commercial
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RESULT 6
CPSA_BOVIN STAN
ID CPSA_BOVIN STAN
AC Q10569;
AC Q10569;
AC Q10569;
CPSA_BOVIN STAN
CPSA_BOVIN STAN
AC Q10569;
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SIGNAL 27 380
CHAIN 27 343
DOMAIN 27 343
TRANSMEM 344 363
DOMAIN 364 380
DISULFID 145 155
DISULFID 184 197
CARBOHYD 215 215
CARBOHYD 215 215
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PROSITE; PS01356;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR,
                                                                                   CHARACTERIZATION.

CHARACTERIZATION.

CHARACTERIZATION.

CHARACTERIZATION.

CHARACTERIZATION.

CHARACTERIZATION.

EXECUTION: Bienzoth S., Lang K.M., Christofori G.;

Keller W., Bienzoth S., Lang K.M., Christofori G.;

Keller W., Bienzoth S., Lang K.M., Christofori G.;

Cleavage and polyadenylation factor CPF specifically interacts with pere-mRNA 3, processing signal AAUAAA.";

EMBO J. 10:4241-4249(1991).

EMBO J. 10:42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jenny A., Keller W.; "Jenny A., Keller W.; "Cloning of cDNAs encoding the 160 kDa subunit of the bovine cleavage "Cloning of cDNAs encoding the 160 kDa subunit of the bovine cleavage and polyadenylation specificity factor."; Nucleic Acids Res. 23:2629-2635(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95380277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 KDA SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSHM-----SPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLG---PIPARCFDYEIEIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ITSDGLTIRLEGGVEDNKPVRYSYTROARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPRREKRWSEWASGKVLCLLDPLDGVYNYLAQQRCNLDDTWEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTTLVTATVENETYTLKTTNE----TRQLCFVVRS
   STEP OF THE POLYADENYLATION REACTION.
SUBUNIT: CPSF IS A HETEROTETRAMER COMPOSED
SUBUNITS 160, 100, 70 AND 30 KDA.
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 20. 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keller W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSEW--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=7651824;
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Glycoprotein;
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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Best Local S
Matches 61
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p14917;
01-APR-1990 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
UREASE BETA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE).
UREB OR HPUB OR HP0072 OR JHP0067.
Helicobacter pylori (Campylobacter pylori), and
Helicobacter pylori J99 (Campylobacter pylori J99).
The proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
         Nucleic
                 "Nucleotide sequence of two for urease subunits."; Nucleic Acids Res. 18:362-36
                                            MEDLINE=90221820; PubMed=2326167;
Clayton C.L., Pallen M.J., Kleanthous H.,
                                                                      SEQUENCE FROM N.A.
                                                                                       Labigne A., Cussac V., Courcoux P.;
"Shuttle cloning and nucleotide sequences
genes responsible for urease activity.";
J. Bacteriol. 173:1920-1931(1991).
                                                                                                 genes
                                                                                                                             MEDLINE-91161505; PubMed-2001995;
                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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DOMAIN 894 909
SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                            RSVRAFHFDKAAA-----SVLTTSMVTMEPGYLFLGSRLGNSLLLKYTEKLQEPPASTAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLVASLGLLAGGSSA--SAAEEAFDLWNECAKAC-----VLDLK------DGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity 25.7
61; Conservative
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                 18:362-362(1990)
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                                  genes
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Pred. No. 1
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                                                                                                                                                                                                                                                                   PRT;
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                                   from
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12;
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                                                                                                           of Helicobacter
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                                   pylori
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PIR; S07885; URKCBP.
PIR; B38537; B38537.
PIR; B41502; B41502.
HSSP; P18314; IFWE.
TIGR; HP0072; TIGR;
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SEQUENCE OF 1-20.
MEDCINE-90264448; PubMed-2188975;
MEDLINE-9026444B; PubMed-2188975;
Dunn B.E., Campbell G.P., Perez-Perez
Dunn B.E., Campbell G.P., Perez-Perez
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Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doi alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doi smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Smith D.R., Vos Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vov
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MEDLINE=97394467; PubMed=92
                                                                                                                      PROSITE; PS00145; UREASE_2; PROSITE; PS01120; UREASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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Pfam; PF00449; urease; 1.
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CATALYTIC ACTIVITY: UREA + H(2)O = CO(2) + 2 NH(3 COFACTOR: EACH CHAIN BINDS TWO NICKEL IONS. SUBUNIT: CONSIST OF TWO SUBUNITS (ALPHA AND BETA) SIMILARITY: BELONGS TO THE UREASE FAMILY.

CAUTION: IN HELICOBACTER THE BETA SUBUNIT IS WHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L; M60398; AAA25021.1; -.

X17079; CAA34933.1; -.

A08818; CAA00811.1; -.

L; A07398; CAA0063.1; -.

L; AE000529; AAD07143.1; -.

AE001446; AAD05651.1; -.
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Best Local Similarity
Matches 41; Conser
                                              MEDLINE-9414054; PubMed-8307567;

X MEDLINE-9414054; Naragogeos D., Theodorakis K., Michaelidis M.T.,

A Modi W.S., Furley J.A., Jessel M.T., Papamatheakis J.;

A Modi W.S., Furley J.A., Jessel M.T., Papamatheakis J.;

A Modi W.S., Furley J.A., Jessel M.T., Papamatheakis J.;

A Modi W.S., Furley J.A., Jessel M.T., Papamatheakis J.;

M. Isolation of the chuman axonal localization of the gene

"Isolation of the chuman axonal plycoprotein TAG-1.";

Genomics 18:562-567(1993).

L. Genomics 18:562-567(1993).

L. Genomics 18:562-567(1993).

L. Genomics 18:562-567(1993).

Genomics 18:562-567
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Q02246;
01_JUL-1993 (Rel. 26, Created)
01_JUL-1993 (Rel. 26, Last seque)
15_JUL-1999 (Rel. 38, Last anno)
AXONIN-1 PRECURSOR (AXONAL GLYC)
GLYCOPROTEIN 1)
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Hasler T.H., Rader C., Stoeckli E.T.,
"CDNA cloning, structural features, an
"DNA cloning, structural features, an
human TAG-1/axonin-1.";
Eur. J. Biochem. 211:329-339(1993).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAX1 OR TAG1.
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             copyright.
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annotation update)
GLYCOPROTEIN TAG-1)
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25; Mismatches
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Catarrhini; Hominidae
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PIR; S28830; S28830.
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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EMBL; Z29337; CAA82536.1;
PIR; S32777; S32777.
PIR; S44049; S44049.
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SEQUENCE FROM N.A.
MEDLINE=97474254; PubMed-9335278;
Kuo Y.-P., Thompson D.K., St Jean
"Characterization of two heat sho
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                                                                                                                                                                                                                        8 (Rel. 36, Created)
8 (Rel. 36, Last seque
8 (Rel. 36, Last anno
SUBUNIT 1 (HEAT SHOCK
                                                                                                                                                                                                                           SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TNGQ-----GVLHYSMVLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77746
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                                                                                                                                                   (Haloferax volcanii); Halobacteriales; Ha
     heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                        sequence update)
annotation update)
SHOCK PROTEIN CCT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85.5; D
Pred. No. 6.2;
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTLAISHAGVSVVMAQTQPRREK 210
                                                                                                                                                                                                                                                                                                                                                    PRT;
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                            A., Charlebois
     genes
                                                                                                                                                                                                                                                                                                                                                    560
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                                                                                                                                                     Halobacteriaceae;
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opp (1967) strain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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     Haloferax
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                              R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                            Daniels
  volcanii:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 68
                                                                                                                                                     Haloferax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marburg
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RESULT 11
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Best Local :
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01-FEB-1996 (Rel. 3
01-FEB-1996 (Rel. 3
NUCLEOPROTEIN (NUCL
                                                                                                                                                                                                                                     VNUC_MABVM
P27588;
01-AUG-1992
            J. Gen. Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00118; cpn60_TCP1; 1.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00750; TCP1_1; 1.
PROSITE; PS00751; TCP1_3; 1.
PROSITE; PS00995; TCP1_3; 1.
Chaperone; ATP-binding; Multigene family; Heat shock.
SEQUENCE 560 AA; 58925 MW; 88B73B2AD70DC341 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        model system for transcription regulation
J. Bacteriol. 179:6318-6324(1997).
-i- FUNCTION: MOLECULAR CHAPERONE; BINDS U
VITRO, AND HAS A WEAK ATPASE ACTIVITY
-i- SUBUNIT: FORMS AN OLIGOMERIC COMPLEX C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
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HSSP; P48424; 1ASX
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                                      viruses.
                                                   comparison to
                                                            SEQUENCE FROM N.A.
MEDLINE=92166742; PubMed-1538192;
Sanchez A., Kiley M.P., Klenk H.D.,
"Sequence analysis of the Marburg v:
                                                                                                                               NCBI_TaxID=33727;
                                                                                                                                             Filovirus
                                                                                                                                                         Viruses;
                                                                                                                                                                    Marburg
                                                                                                                                                                                     Z
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REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 LLAGGSSASAAEEAFDLWNECAKACVLDLK--DGVRSSRMSVDPAIADTNGQGVLHYSMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                    DL-----
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                                                                                                                                                                                                                                                                                                                                                                                    DQLVEVGAD----AVFV----
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                                                                                                                                                                       virus
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                                                                                                                                                         SSRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                   Ebola
                                                                                                                                                                    (strain
                                                                                                                                                                                                (NUCLEOCAPSID
                                                                                                                                                        (strain Musoke).
negative-strand
                          73:347-357(1992)
                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                             33,23
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19.2%;
                                                   Virus
                                                                                                                                                                                                           Last sequence up
                                                                                                                                                                                                                                       Created)
                                                   and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      -GDGIDDMAQHY----
                                                                                                                                                                                                 PROTEIN)
                                                                                                                                                                                                                                                                                                                                    --KRLARATGGRVVSSLDDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84.5;
Pred. No. 5
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCP-1 CHAPERONIN FAMILY
                                                                                                                                                         viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E; BINDS UNFOLDED POLYPEPTIDES ACTIVITY (BY SIMILARITY). COMPLEX OF EIGHT-MEMBERED RIN
                                                                 virus nucleoprotein gene:
                                                   non-segmented
                                                                                                                                                                                                                          update)
                                                                             Feldmann
                                                                                                                                                                                                                                                                 692
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                                                   negative-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                           Filoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M72714; AAA46563.1; ALT_SEQ.
EMBL; Z12132; CAA78114.1; -
PIR; JQ1408; VHIWMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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005514;
30-MAY-2000
30-MAY-2000
30-MAY-2000
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SEQUENCE 692 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
THIAMINE-MONOPHOSPHATE KINASE (EC 2.7.4.16) (THIAMINE-PHOSPHATE
                                                                                                                                                                                                   the Bacillus subtilis chromosome.";
Microbiology 143:1861-1866(1997).
-i- CATALYTIC ACTIVITY: ATP + THIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168 / MARBURG;
MEDLINE=97346038; PubMed=92
Sadaie Y., Yata K., Fujita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                  Ogasawara N.;
"Nucleotide sequence and analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341
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Subtilist; BG10693; thiL.
Thiamine biosynthesis; Transferase; Kinase.
SEQUENCE 325 AA; 35884 MW; 95D2D6762CFDBCCB CRC64;
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15-JUL-1998
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MEDLINE-9728432; PubMed-9074510;
Feltri M.L., Arona M., Scherer S.S., Wrabetz L.;
Teltri and sequence of the cDNA encoding the beta 4 integrin subunit in rat peripheral nerve.";
Gene 186:299-304(1997).
Gene 186:299-304(1997).
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
1NTEGRIN BETA-4 PRECURSOR (GP150) (CD104).
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                                                                                                                                         -i- FUNCTION: INTEGRIN ALPHA-6/BETA-4 MAY MEDIATE ADHESIVE AND/OR MIGRATORY FUNCTIONS OF EPITHELIAL CELLS (BY SIMILARITY).
-i- SUBUNIT: DIMER OF AN ALPHA AND BETA SUBUNIT. BETA-4 ASSOCIATES WITH ALPHA-6 (BY SIMILARITY).
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PF00362; integrin_B; 1.
S; PR00014; FNTYPEIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d and this statement is not remove requires a license agreement (S an email to license@isb-sib.ch).
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                 PRECURSOR
                                                                                                STANDARD;
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               Last sequence up
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SOR (EC 3.5.2.6)
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BY SIMILARITY.
INTEGRIN BETA-4.
EXTRACELLULAR (POTENTIAL).
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PIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.
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Pred. No. 43;
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CYSTEINE-RICH REPEATS.
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REFERENCE DE LA CONTRACTOR DE LA CONTRAC
Banerjee S., I "Role of the of structure of Biochemistry [10]
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STRALN-NCTC 9789; TRANSPOSON-TD552;
MEDLINE-91014696; PubMed-2170815;
Rowland S.J., Dyke K.G.H.;
"TD552, a novel transposable element Mol. Microbiol. 4:961-975(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene.
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"Refined
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"Nucleotide sequence of the blaz gene
beta-lactamase transposon Tn4002.";
Nucleic Acids Res. 17:8854-8854(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Staphylococcus group; Staphylococcus NCBI_TaxID=1280;
                                                                                                                                                                  aureus PC1 at
J. Mol. Biol.
                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). MEDLINE=91171295; Pubmed=2005620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-76135454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence and expression Staphylococcus aureus plasmid pI258 subtilis, and Staphylococcus aureus
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STRAIN=PC-1; PLASMID=p1258;
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                                                                                                                           CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lin J.R., Murray C.L., Rabinowitz J.C.; features in the ribosome binding site sequence features aureus beta-lactamase gene."; Chem. 256:11283-11291(1981).
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35454; PubMed=1218078;
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                     Pieper U., Kapadia G., Pannell L.K., Fomega-loop in the activity, substrate class A beta-lactamase.";
37:3286-3296(1998).
                                                                                                                                                                                                                                                                                                                                                                                                 Moult
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217:701-719(1991).
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PubMed=3107125;
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                                                                                                                                                                                        resolution.";
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EMBL; X16471; CAA34491.1; ...
EMBL; M15526; AAA982391; ...
EMBL; X52734; CAA36953.1; ...
PIR; A01002; PNSAP.
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"Relocation of the catalytic carboxylate group in class A beta-
lactamase: the structure and function of the mutant enzyme
Glu166-->Gln:Asn170-->Asp.";
Protein Eng. 12:573-579(1999).

-1- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)0 = A SUBSTITUTED I
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MEDLINE=99365425; PubMed=10436083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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-!- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY
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PDB; 1KGG; 28-MAY-99.
PDB; 1KGG; 28-MAY-99.
Interpro; IPR00187; -.
Interpro; IPR001466; -.
Pfam; PP00144; beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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30-JAN-94
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30-APR-94
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                                                          "The control region of the pdu/cob typhimurium.";
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                                                                                                                             Salmonella.
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MEDLINE-98012959; PubMed-9352910; Bobik T.A., Xu Y., Jeter R.M., Otto K.E., Roth J.R.; Propanediol utilization genes (pdu) of Salmonella t genes for the propanediol dehydratase.";
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                                                       Bacteriol. 176:5474-5482(1994).
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Q28733 oryctolagus
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Q955w4 helicobacte
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Q16921 aedes aegyp
Q48490 bacteriopha
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## ALIGNMENTS

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V1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 44.1 KDA PROTEIN.
SCF51.09C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9RJS6;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycesaceae; Streptomyces.
NCBI_TaxID=1902;
                                                 Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; ast of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL132707; CAB59707.1; -.
InterPro; IPR002106; -.
InterPro; IPR002504; -.
                                                                                                                                                           STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                STRAIN=A3(2);
Cerdeno A.M.,
                                                                                                                                                                                                                                                                                     Seeger K.J., Harris D.;
Submitted (OCT-1999) to
                        Pfam; PF01513; DUF15; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
                                                                                                                                                                                                                     Submitted
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Hypothetical protein. SEQUENCE 416 AA; 4
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MEDIINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. Hickey M.J., Brinkman F. S.L., Hufnagle W.O., Kowalik D.J., Lagrou Hickey M.J., Brinkman F. S.L., Hufnagle W.O., Kowalik D.J., Lagrou Y. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an "Complete genome sequence", Nacutre 406:959-964 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176
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3317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
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                                                                                                       3257
                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 4180 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001969; -. PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLEKLSRDRQISVGVYI----AGRLLASYS-----ADALLVATPTGSTAYSFAAGGPV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V--PIGHEKPSNIKVFIHELNAGNQLSHMSPTYTIEMGDELLAKLARDATFFVRAHESNE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLTLRASRLLEIPAEMEALLRY-----GRGPLLPPPRVRTDCESGDEWGIALNVTALNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTLGGDGTFLRGARLAAENDALILGVDLGRVGFLTEVPAPAVRSALDAVRDGGLEPESRM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IERVGLVVHGGREGAAEAAREVREWCDENAVACTDIDVWSDTGRHSAREEVDAAGDPDLV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNYLAQQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MQP-----TLAISHAGV--SVVMAQTQP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADTNGQGVLHYSMVLEGGNDALKLAID-----
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                                                                                                                                                   LKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
75; Conserv
  DLNVRIGGEVNPSREARATQTYSSSG---FDGLYSGG----
                                                 -LTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHEL-NAGNQLSH 153
                                                                                                     LGGGNLSMRTGGDAGNIAPRGDGSIPSSGNLNPRSQGLVLAVAGTGRLTSDGALQLGGGG
                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                        7.1%;
27.8%;
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Last
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                WW.
                                                                                                                                                                                                                                        Score 93.5;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision; Pseudomonadaceae;
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annotation
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                                                                                                                                                                                                                                                                         2;
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                ----TIHDLQGALINLRG 3364
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                                                                                                                                                                                                                                                                      Length 4180;
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                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230
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                                                                                                                                                                                                                             Gaps
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RESULT
Q9S5W2
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Best Local S
Matches 42
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01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9S5W2;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanahashi T., Kita M., Kodama T., Sawai N., Yamaoka Y., Mitsufuj
Katoh F., Kashima K., Imanishi J.;
"Comparison of PCR-restriction fragment length polymorphism and
direct sequencing method for differentiating Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UREB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UREASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9S5W2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154
                                                                                                               Q9DDT1;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-KP72B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00449; urease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB028036;
HSSP; P18314; 2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.";
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01120; UREASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002467; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                Brachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota; Metazoa; Chordata; Craniata; Ver
Actinopterygii; Neopterygii; Teleostei; Euto
Cypriniformes; Cyprinidae; Rasborinae; Danio
                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                      Q9DDT1
                                      NCBI_TaxID=7955;
                                                                                            S
                                                                                                    PYRUVATE
  Yoder J.A., Lit
                     SEQUENCE FROM N.A.
                                                                                                                                                                                                       132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SASLYSGALGGIDPRYDTLLRDPA-EVRSRDA--FSPTLASSTGGLTLVAGDTGMRLETR
                                                                                                                                                                                                                                                                DGLTIRLEGGVEPNKFVRYSYTRQARGSWSLNWLVFIGHEKPSNIKVFIHELNAGNQLSH
                                                                                                                                                                                                                                                                                    DMQDGVKNN-LSVGPATEALAGEGLI----VTAGG-----IDTHIHFISPQQIPTAFA
                                                                                                                                                                                                                                                                                              SGYTTMIGGGTGPADGT--NATTITPGRRNLKWMLRAAEEYSMNLG-FLAKGNASNDAS-
                                                                                                                                                                                                                         MSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHA
                                                                                                                                                                                                                                                                                                                          l Similarity
42; Conserv
                                                                                                      CARBOXYLASE.
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220 i
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                                                                                                                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                             Conservative
    Litman G.W.;
lsh fth1, slc
                                                                                                                                                        PRELIMINARY;
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22602 MW;
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     slc3a2, men1,
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13,
16,
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                                                                                                                                                                                                          -GAIGLKIHESWGTTPS-AINHA
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                       Score 92.5; DB pred. No. 0.85;
                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                     Created)
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                                                                                                                                                           PRT;
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                                                                                                                                                            1180
                                                         Danio
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     fgf3 and
                                                                 vertebrata; Euteleostomi;
Euteleostei; Ostariophysi
                                                                                                                                                            B
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       cycd1
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                                                                     Ostariophys1;
        genes define two
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RESULT
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q38139;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                      MEDLINE=94172631; PubMed=8126723; Peder G., Alon Pedre X., Weise F., Chai S., Lueder G., Alon "Analysis of cis and trans acting elements r of DNA replication in the Bacillus subtilis J. Mol. Biol. 236:1324-1340(1994).

EMBL; X67865; CAM48050.1; -.

EMBL; X67865; CAM48050.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regions of conserved synteny chromosome 11q13.";
Gene 0.0-0(2001).
EMBL; AF295372; AAG37836.1;
SEQUENCE 1180 AA; 129884
                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses,
Lambda phage group.
NCBI_TaxID=10724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q38139
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriophage
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                   ELLAKLARDATFFVRAHESNEMQPTLAISHA
                                                                                  RYSYTROARGSWSLNWLVPIGHEKPSNIKV-----FIHELNAGNQLSHMSPIYTIEMGD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CVLDLKD--GV---RSSRMSVD-----PAIA----DTNGQGVLHYSMVLEGGNDAL
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17; Mismatches
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Q28733; Q28736;
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Q1-NOV-1996
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SEQUENCE
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Mueller-Seitz M., Kaupmann K., Labeit S., Jockusch "Chromosomal localization of the mouse titin gene "muscular dystrophy with myositis' and nebulin gen 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92258380; PubMed-1582406; Labeit S., Gautel M., Lakey A., Tri "Towards a molecular understanding EMBO J. 11:1711-1716(1992).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
01-MAR-2001
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                                                                                                                                                                                   VSVV----MAQTQPRREKRWSEWASGKVLCLLDPLDGVYNYLAQ
                                                                                                                                                                                                                      EGCSYYFRVTAENEYGIGLAARTADPIKVAEVPQPPGKITVDDVTRNSVSLSWTKPEHDG
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                                                                                                                                                                                                                                                                                                                       YSYTROARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNOLSHMSPIYTIEMGDELLAKLA 171
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Metazoa; Cl
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531 AA;
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l (TrEMBLrel.
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Rodentia;
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Pred. No. 5
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Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90238553; PubMed=2129545; (Labeit S., Barlow D.P., Gautel M., (Francke U., Leonard K., Wardale J., "A regular pattern of two types of of titin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Labeit S., Gautel M., Lakey A., Tr.
"Towards a molecular understanding
EMBO J. 11:1711-1716(1992).
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EMBL; X17329; CAA35207.1;
HSSP; P56276; 1TLK.
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SEQUENCE
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Pfam; PF00047; ig; 15.
PRINTS; PR00014; FNTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 345:273-276(1990).
-!- SIMILARITY: TO IMMUNOGLOBULIN
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  Q10466 PRELIMINARY; PRT; 26926 AA.
Q10466;
Q10466;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN).
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PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00726; LEXASERPTASE.

PROSITE; PS00933; FGGY_KINASES_1; UNKNOWN_1.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

PROSITE; PS00039; IG_MHC; UNKNOWN_1.

PROSITE; PS0043; PEROXIDASE_1; UNKNOWN_1.

PROSITE; PS50011; PROTEIN_KINASE_DOW; 1.

PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.

SMART; SM00408; IGC2; 1.
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EMBL; X83270; CAA58243.1
EMBL; X64697; CAA45938.1.
EMBL; X64697; CAA622188.1
EMBL; X64699; CAA62218.1
EMBL; X64699; CAA45940.1;
                                                                                                                                                                                              Interpro; IPRO00129; ...
Interpro; IPRO00282; ...
Interpro; IPR000577; ...
Interpro; IPR000719; ...
Interpro; IPR0007149; ...
Interpro; IPR001777; ...
Interpro; IPR001777; ...
Interpro; IPR003016; ...
Interpro; IPR003015; ...
Interpro; IPR003015; ...
Interpro; IPR003015; ...
Interpro; IPR003598; ...
Interpro; IPR003598; ...
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 22277-25376 FROM MEDLINE=92258380; PubMed=1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1976-2014 FROM Labeit S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1994) to the
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Pfam; PF00047; ig; 95.
Pfam; PF00069; pkinase;
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Muscle protein; Cytoskeleton; Str
Serine/threonine-protein kinase;
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SARTOMERES. MAY HAVE PROPEIN KINASE ACTIVITY.

SALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN AN ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFORM
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TISSUE SPECIFICITY:
SIMILARITY: TO THE (
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   Cytoskeleton; Structural protein; Calm
e-protein kinase; Alternative splicing;
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01-MAY-2000 (TrEMBLrel.
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                                                       Submitted (MAY-1999) to the EMBL; AB028038; BAA78630.1; HSSP; P41020; 1UBP.
                                                                                           Tanahashi T., Kita M., Kodama T., Sawai N., 1
Katoh F., Kashima K., Imanishi J.;
"Comparison of PCR-restriction fragment length
direct sequencing method for differentiating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter
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                                              InterPro;
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Q93538;
Q1-FEB-1997
O1-FEB-1997
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Forntians B., Walkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F20D1.6
F20D1.6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
EMBL; Z78542; CAB01748.1; -.
SEQUENCE 915 AA; 104584 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
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                                              134
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                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                              300 NYSSYWNIKMKSTKSSLLGVLDEILGVYREDTRKAIRSDLNCALILGKHYTQ-KELPNAF
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                                                                                                                                                                                                                                                                                                                                            EMGDELLAKLARDATFFVRAHESNEMQPTLAISHA 195
                                                                                                                                                                                                                                          -----WN---ECAKACVLDLKDGVRS-SRMSVDPAI-ADTNGQGVL--HYSMVLEGGNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTGPADGT -- NATTITPGRRNLKWMLRAAEEYSMNLG-FLAKGNASNDAS----
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AESDNESLAHELNMLNAASMSENQLSDDELVNNVKLDTLFNYKNPKSANTFLAPYKCAKK
                                              KPSNIKVFIHELN-----AGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEM
                                                                                               QKLTINSASEVKIGKHAETEDSGT
                                                                                                                                                LKLAIDNALSI-----
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22.7%;
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25.2%;
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                                                                                                                                             -TSDGLTIRLEGGVEPNKPVRYSYTROARGSWSLNWLVPIGHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                             47;
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Last sequence update)
Last annotation updat
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Pred. No.
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                                                                                               - NGPMPPALMK
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                                                                                                                                                                                                                                                                                                                                                                                             96;
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Matches 50
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Q1-NOV-1996 (TrEMBLrel. 01,

Q1-NOV-1996 (TrEMBLrel. 16,

Q1-MAR-2001 (TrEMBLrel. 16,

PYRUVATE CARBOXYLASE.
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1 - COFACTOR: BIOTIN (BY SIMILARITY).

EMBL: L36530; AAB64306.1;

HSSP: P10802, 1IYU.
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Aedes aegypti (Yellowfever mosquito).
Aedes aegypti (Yellowfever mosquito).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97218699; PubMed=9066123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001882; -.
InterPro; IPR00379; -.
Pfam; PF00289; CPSase_L_chain;
Pfam; PF00364; biotLn_lipoyl; .
Pfam; PF00682; MGG-like; 1.
Pfam; PF02436; PYC_OADA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biotin; Pyruvate
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048490;
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                                                                                                                                                                                                                                                                                                                            THILCIKDMAGLLKPQAAKLLIAAIREKHPDVPIHIHTHDTSGAGVASMLACAEAGADVV
                                                                                                                                                                                                                                                                                                                                                                      ----CVLDLKD------GVRSSRMSVDPAI--ADTNGQGVLHYSMVLEGGNDAL 81
                                                                                                                                                                                                                                   DVAVDSMSGMTSQPSMGAVVASLQGTPLDTGLNLRDISEYSAYWEQTRTLYA----
                                                                                                                                                                                                                                                                KLAIDNALSITSD---GLTIR-----LEGGYEPNKPVRYS-YTRQARGSWSLNWLVPI-
                                                                                                                                          {\tt CTTTMKSGNADVYLNEIPGGQYTNLQFQAYSLGLGDFFEDVKKAYREANLLL}
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IPR000891; -.
IPR000901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001882; -. IPR003379; -.
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                                PRELIMINARY;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 88;
Pred. No.
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Best Local :
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
COMPLETE NUCLECTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Alonso J.C., Luder G., Stiege A.C., Chai S., W
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
EMBL; x97918; CA66538.1; -.
SEQUENCE 311 AA; 35943 MW; 1BD3468DA07DAF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage SPP1.
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O29117 O2903; O29034; O29017; O29037; O29017; O29037; 
                           Interpro: IPR001777; -.
Interpro: IPR003006; -.
Interpro: IPR003598; -.
Interpro: IPR003598; -.
Pfam; PF00041; fn3; 3.
Pfam; PF00047; i9; 2.
PRINTS; PR00014; FNYYPEIII.
SMART; SM00408; IGC2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93365278; PubMed=8359022; Filtz J.D., Wolff J.A., Greaser M.L.; Wolff M.A., Greaser M.L.; "Characterization of a partial cDNA clone encoding muscle titin: comparison with rabbit and mouse skel sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITIN (CONNECTIN) (FRAGMENT).

Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comp.
                                                                                                                                                                            EMBL; M97767; AAA02948.1;
EMBL; D85840; BAA12876.1;
EMBL; D85841; BAA12877.1;
                                                                                                                                                                                                                                                                        Tanabe R., Muroya S., Nakajima I., Chikuni K., "Skeletal muscle connectin primary structures a species and muscle type."

J. Rood Sci. 62:451-461(1997).

-:- SIMILARITY: TO IMMUNOSLOBULIN AND MAJOR HIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 62-121 AND
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                      SMART; SM00408; IGc2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYSYTRQARGSWSLNWLVPIGHEKPSNIKV-----FIHELNAGNQLSHMSPIYTIEMGD
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J databases
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                                                                                                                                                                                                                                                                                         HISTOCOMPATIBILITY COMPLEX
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as related
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Sus.
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NON_TER
SEQUENCE
                                            Submitted (MAR-2000) to the EMBL
EMBL; ACCO04809; AAF40445.1; -.
InterPro; IPR001296; -
Pfam; PF00534; Glycos_transf_1;
SEQUENCE 1064 AA; 119675 MW;
                                                                                                                                                                                                                                                                                        STRAIN-CV. COLUMBIA; Vysotskala V.S., Schwartz J.R., Torlumi M., Yu G., Kwan A Vysotskala V.S., Schwartz J.R., Torlumi M., Yu G., Kwan A Li J., Kremenetskala I., Luros J., Araujo R., Au M., Bredd Buehler E., Conway A., Dewar K., Feng J., Kim C., Kurtz D Palm C., Shinn P., Sun H., Davis R., Ecker J., Federspiel
                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
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STRAIN-CV. COLUMBIA;
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                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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itted (JUN-1998)
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Last sequence Last anno
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dicots; Rosidae;
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Bredel V.,
urtz D., Li Y.,
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e; eurosids II;
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PE PROSITE; PS01120; UREASE_1; 1

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SEQUENCE 220 220
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Q9WXL2;
01-NOV-1999
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Tanahashi T., Kita M., Kodama T., Surres
Katoh F., Kashima K., Imanishi J.;
"Comparison of PCR-restriction fragment length polymorphis
"Comparison of PCR-restriction fragment length polymorphis
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HSSP; P18314; IFWB.
InterPro-
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Tanahashi T.,
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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Pred. No. 3.1;
24; Mismatches
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Page 8

Search completed: November 13, 2001, 14:34:07 Job time: 433 sec

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Result
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110987654
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AAB3 7791
AAB3 7791
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## ALIGNMENTS

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                                                                                                                                             Key
                                       14-OCT-1993.
                                                                                                                                                                                    autoimmune dysfunction.
                                                                                                                                                                                                                                                                                                    AAR42060;
30-MAR-1992;
                   26-MAR-1993;
                                                           W09319777-A.
                                                                                        Region
                                                                                                             Protein
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                                                                                                                                                                Homo sapiens
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92US-0860710
                   93WO-US02938
                                                                      /note= "Transmembrane region"
                                                                                                /note= "Signal peptide 21..553 /note= "Mature hIl-lR"
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protein is by such a distance that each component of the fusion protein is capable of folding into the secondary or tertiary structure required capable of folding into the secondary or tertiary structure required to the secondary or tertiary structure required capable of diagnosis and assays for conditions mediated by TNF or IL-1, therapy, diagnosis and assays for conditions mediated by TNF or IL-1, therapy, diagnosis and assays in which both TNF and IL-1 play a causitive particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAR42058-59 repressent human tumour necrosis factor receptor (TNF-R) and the sequences in AAR42060-61 represent human interleukin-1 receptor (IL-1R). These sequences were used in the production of a fusion protein which conformed to one of the formulae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New fusion protein tumour necrosis factor and human interleukin-l receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-336592/42
N-PSDB; AAQ49933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 61-64; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                           AAP92001 standard; protein; 569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune dysfunctions.
                                                                                                                                                                       кеу
                                                                                                                                                                                                                                    Human interleukin-1 receptor; IL-1R; human
                                                                                                                                                                                                                                                                  Derived sequence of human interleukin-1 receptor (IL-1R) gene.
                                                                                                                                                                                                                                                                                                  07-FEB-1990
                                                                                                                                                                                                                                                                                                                                AAP92001;
30-APR-1984;
21-DEC-1984;
                                                                                                                                                        Protein
                                                                                                                                                                                                       Homo sapiens
                                               24-NOV-1988;
                                                                              31-MAY-1989
                                                                                                             EP381296-A.
                                                                                                                                        Region
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322 migicvtltvii 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF-R-linker-TNF-R-linker-IL-1R
IL-1R-linker-TNF-R-linker-TNF-R or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                    (first entry)
 84US-0605540
84US-0684560
                                                88EP-0311150
                                                                                                                                         Location/Qualifiers
18
337..356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                            T-cell line clone 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT
AAP90330
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Best Local Similarity
""" 8; Conserv
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                                                                                                                                                                                                                                                   XXX OS XXX DE XXX
Derived sequence of the coding region of a cDNA encoding human IL-IR. The Protein feature = N-terminus of mature protein. The Region feature = transmembrane region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA coding for mammalian interleukin-receptor used for obtaining protein and antibodies for diagnosis and therapy involving immune or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dower SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; figure 5A-5C; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAN90118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMU-) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                            Clone; interleukin-1 receptor; human; immune regulator;
                                                                                                                                                                                                                                                                                                                                                      01-NOV-1989 (first entry)
                                                                                                                                                                                                                                                                                                                                                                          AAP90330;
                                                                                                                                                                                                                                                                                                                                                                                              AAP90330 standard; protein;
                                                                                     DNA sequences encoding mammalian interleukin-1 receptors used to regulate immuno or inflammatory responses or detect IL-1 and its receptor interaction
                                                                                                                                                                                                                                                               W08904838-A
                                                                                                                                                                                                                                                                                  Murine
                                                                                                                                                                                                                                                                                                                                  Human interleukin-1 receptor
                  Peptide of human interleukin-1 receptor (see AAN90031). This is used in human and veterinary medicine to regulate or inflammatory responses, and to detect and study IL-1 molecules and their receptors
                                                                                                                                                                                OWMI)
                                                                                                                                                                                                                        04-NOV-1988;
                                                                                                                                                                                                                                                                                                     inflammatory
                                                                                                                                N-PSDB;
                                                                                                                                                                                                    25-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                              338 migicytltvii 349
                                                                                                                                           WPI; 1989-178365/24.
                                                                                                                                                            Dower SK,
Sequence
                                                                    Disclosure; Table 4a-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LIGICVAVTVAI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1989-159346/22.
                                                                                                                                                                                ) IMMUNEX CORP
                                                                                                                                AAN90031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569 AA;
                                                                                                                                                               March CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                    response.
                                                                                                                                                                                                     87US-0258756
                                                                                                                                                                                                                         88WO-US03926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sims JE,
                                                                                                                                                                Sims
                                                                        51pp; English.
                                                                                                                                                                JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB pred. No. 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Urdal
                                                                                                                                                                 Urdal DL;
                                                                                                                                                                                                                                                                                                                                                                                                 AA
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                                               immune
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Best Local Similarity
Whiches 8; Conservi
        This protein is the soluble human interleukin-1 receptor (IL-IR). by mutating codon 336 (AAG) of the CDNA encoding IL-IR (AAG71901), to form a stop codon (TAG) a truncated receptor, comprising the extracellular domain only, is generated. This truncated receptor retains its ability to bind interleukin-1 but is released extracellularly and therefore is inactive in signal transduction. The methods of the invention are useful for preventing the development of arthritis and for therapeutic use, eg. for repairing and regenerating the connective tissue. The gene is also useful in a compound for parenteral administration for prophylaxis or treatment. (Also see AAR59091 for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human interleukin-1 receptor; I1-1R; truncated; connective tissue; prevention; arthritis; therapy; repairing; regenerating; ligament; tendon; cartilage; synovium; prophylaxis; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human interleukin-1 receptor
                                                                                                                                                                                                                                                                                                                     07-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR59090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR59090 standard;
                                                                                                                                                                     Methods for introducing genes into connective tissue treating connective tissue disorders, e.g. arthritis
                                                                                                                                                                                                                                                                                             08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                      WO9420517-A
                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                         N-PSDB; AAQ71901
                                                                                                                                                                                                                                                                     (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                                                                              15-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 migicvtltvii 349
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                                                                                                                                                                                                                       1994-302952/37
interleukin-1 receptor).
                                                                                                                                            Page 49-51; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                            Evans CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                             93US-0027750
                                                                                                                                                                                                                                                                                                                     94WO-US02414
                                                                                                                                                                                                                                                                                                                                                                                                       /note-
357..5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "extracellular domain"
44..96
142..196
248..312
                                                                                                                                                                                                                                                                                                                                                                                                                                 336..356
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "a truncated receptor
    mutation of the codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                           . 569
                                                                                                                                                                                                                                            Glorioso JC,
                                                                                                                                                                                                                                                                                                                                                                                             "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                    "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                           to a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.;
                                                                                                                                                                                                                                            Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        is generated by for this residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2:
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                                                                                                                                                                                  cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT
AAR60870
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Best Local Similarity
Thehes 8; Conserv
Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sox
       The amino acid sequence of the human interleukin-1 (IL-1) receptor (IL-1R) encoded by the insert fragment R3A. The gene (AAQ73764) encodes CC a 65 kD protein precursor which is converted to 63.5 kD protein. The CC protein then undergoes glycosylation to produce a protein of around CC 82 kD. The gene was isolated from a cDNA library, derived from RNA from CC a human T-cell line (designated clone 22), by using a probe prepared CC from the murine IL-1R gene sequence (AAQ73762). Nine positive clones CC complete coding region of the human IL-1R. The purified IL-1 receptor, CC as part of compositions, can be used for the diagnosis of IL-1 or its CC receptors. The receptor will also be useful for the production of CC antibodies used in diagnosis and therapy. In addition, the purified IL-1, CC thereby providing means for regulating the immune or inflammatory CC activities of IL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine; interleukin-1; receptor; glycoprotein; human; IL-1-alpha; expression vector; antibody; diagnosis; therapy; IL-1; IL-1R regulation; regulate; immune; inflammatory; activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                 Recombinant cell lines expressing interleukin-1 receptor proteins - also antibodies and compositions for use in diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-1987;
25-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR60870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR60870 standard;
                                                                                                                                                                                                                            Example 5; Fig 5; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                              24-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IL·1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 migicytltvii 349
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                                                                                                                                                                                                                                                                                                                       1994-343308/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569
                                                                                                                                                                                                                                                                                                                                                   March CJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                       87US-0125627
88US-0160550
                                                                                                                                                                                                                                                                                                                                                                                                                                              88EP-0311150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= mature human IL-1 receptor
337..356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
18..569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                   Sims
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42;
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                                                                                                                                                                                                                                                                                                                                                   Urdal DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain
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15;
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Sequence

569

ΑĄ.

Best Loc Matches Query Match

Local

Similarity 8; Conserv

Conservative

2;

Mismatches

75 66

.7%;

Score 42; DB Pred. No. 15;

15; 'n

Length 569 Indels

0;

Gaps

0

0;

Query Match

75.0%;

Score 42;

DВ

18;

Length 569;

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RESULT
AAR90376
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                     And Human interleukin-1 receptor I-type (IL-IR) preferably comprises of CC amino acids 1-319, and more preferably is a soluble protein CC comprising of amino acids 1-312. It is useful as a bone resorption CC comprising of amino acids 1-312. It is useful as a bone resorption CC inhibitor and can be administered intravenously or intramuscutiarly. CC A pharmaceutical composition, containing IL-IR as an active A pharmaceutical composition of treat metabolic diseases of the bone CC ingredient, helps prevent and treat metabolic diseases of the bone CC in the bone, e.g. osteoporosis and hypercalcaemia. The IL-IR is a CC in the bone, e.g. osteoporosis and hypercalcaemia. The IL-IR is a CC superior therapeutic agent to the prior art medications giving a CC more satisfactory effect for metabolic bone diseases caused by CC abnormal bone resorption by inactivating osteoclasts. Bone CC assaying a direct action on osteoclast activity, e.g. by pit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR90376 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR90376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human interleukin-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUL-1996
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338 migicvtltvii 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                         Composition contg. interleukin-1 receptor, or soluble fragment treating and prophylaxis of metabolic bone diseases e.g. osteoporosis or hypercalcemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP687470-A2
                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                   WPI; 1996-041308/05
                                                                                                                                                                                                                                                                                                                             Katoh M,
                                                                                                                                                                                                                                                                                                                                                    (FARH ) HOECHST JAPAN LTD. (FARH ) HOECHST JAPAN KK.
           formation assay
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                                                                                                                                                                                                                   5; Page 5-7; 10pp; English
                                                                                                                                                                                                                                                                                                                             Kitamura K;
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metabolic disease; osteoporosis; hypercalcaemia
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synoviocyte; connective tissue; gene therapy; retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                             The human interleukin-1 receptor (IL-IR) (AAM06541) amino acid sequence can be deduced from a cDNA clone (AAT45876) isolated from a sequence can be deduced from a cDNA clone (AAT45876) isolated from a human T-cell cDNA library. cDNA encoding the extracellular IL-1 binding domain of IL-IR can be generated by PCR (see also AAT45878-79) and incorporated into a retrovirus vector subsequently used to transfect a packaging cell line. Viral particles are produced that can be used to infect synovial cells in culture. Infected cells are then transplanted into the damaged cartilage of a patient. Soluble IL-IR is expressed that binds to and neutralises IL-1 in vivo, preventing degradation of cartilage, as a means of treating arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of a mammalian cartilage defect e.g. arthritis - by re-implanting chondrocyte(s) and synoviocyte(s) contg. DNA encoding a protein to inhibit interleukin-l associated cartilage damage
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                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 77-79; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT45876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 569 AA
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; inflammation; arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is given in a specification relating to novel compositions and methods containing tetracycline or tetracycline-like compounds for treating and/or preventing acute inflammatory responses a diseases. Such diseases include acute inflammatory conditions associate with viral haemorrhagic diseases (including diseases caused by Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses), parasitic diseases, bacterial infections, sepsis, cachexia, autolimnune disorders, acute cardiovascular events, chronic myelogenous leukaemia a disorders, acute cardiovascular events, chronic myelogenous leukaemia a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB37791 standard;
                                                                                                                                                                                                                                                                                                                                                                              transplanted bone marrow-induced graft-versus-host disease, septic immune complex-induced colitis, cerebrospinal fluid inflammation, multiple sclerosis, inflammatory responses associated with trauma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel compositions comprising tetracycline or tetracycline-like compounds for the treatment and/or prevention of acute inflammatory responses and diseases, e.g. septic shock and immune complex-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation; infection; sepsis; cachexia; autoimmune disorder; cardiovascular disorder; chronic myelogenous leukaemia;
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immunomodulator; cardiant; cytostatic; neuroprotective; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human interleukin-1 receptor,
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                                                                                                                                                                                                                                                                                                                                   systemic inflammatory response syndrome (SIRS), adult respiratory distress syndrome (ARDS), acute liver failure, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1999;
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                                                                                                                                                                                                                                                   Sequence
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20-DEC-1990;
23-JUL-1996;
                                                                                                                                                                                                                                                                    The present sequence represents a human interleukin-1 (IL-1) polypeptide. The IL-1 polypeptide is used in the method of the invention. The specification describes a method for inhibiting leukocyte infiltration or cartilage degradation in a joint of a mammal. The method comprises administering a viral vector encoding a protein of interest, such that expression of the protein within the joint results in an inhibition of leukocyte infiltration or cartilage degradation in the joint. This protein is an IL-1 receptor antagonist (IRAP), soluble IL-1 receptor, soluble tumour necrosis factor-alpha (TNF-alpha) receptor. IL-10, or their biologically active fragments or derivatives. The method is used for treating connective tissue disorders by inhibiting leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting leukocyte infiltration or cartilage degradation in mammalian joint, comprises administering a viral vector comprising a nucleotide sequence operably linked to a promoter encoding a protein of interest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A human interleukin-1 (IL-1) receptor polypeptide
           AAB59700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ghivizzani SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; interleukin-1; leukocyte infiltration; cartilage degradation; IL-1 receptor antagonist; IRAP; tumour necrosis factor-alpha receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB30921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB30921 standard;
                                     AAB59700 standard;
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNF-alpha receptor; IL-1.
                                                                                                                                                                                                                                                            infiltration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYPI-) UNIV PITTSBURGH
                                                                                                         338
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                                                                                                                                 1 LIGICVAVTVAI 12
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migicvtltvii
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                                                                                                                                                             Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Columns 47-52; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC86847
                                                                                                                                                                                                                                569
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                          and cartilage degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0027750.
90US-0630981.
96US-0685212.
                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0924376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robbins PD,
                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                          75.0%;
66.7%;
                                     569
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                                                                                                                                                                          Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans
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                                                                                                                                                             Mismatches
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15;
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                                                                                                                                                                                        22;
                                                                                                                                                                                        Length 569
                                                                                                                                                             0;
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Best Local
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20-OCT-1992;
08-MAR-1993;
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27-JAN-1995;
05-DEC-1995;
23-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; interleuk joint pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6156304-A
                                                                                                                                                                                                                                                                                                                                                                                     Producing a protein in a mammalian mammalian host, by administering a nucleic acid encoding the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-2000
                                                                                                                                                                                                                                                                                                           viral vector comprising the coding sequence of the where the protein is expressed in a synovial cell treatment of joint pathologies such as arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-079537/09.
N-PSDB; AAF24245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glorioso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYPI-) UNIV
                                                                                                                                                                                                                                                                                                                                                                     Example 3;
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                       The present invention provides a method of producing a protein in the joint of a mammal, involving the intra-articular administration of a
                                                                                                                                                      AAY07078 standard; Protein; 297
                                                         prostate cancer
                                                                  breast cancer; colon cancer; gastric
                                                                                              Renal cancer
                                                                                                                  02-JUL-1999
                                                                                                                                     AAY07078;
 28-JAN-1999
                    WO9904265-A2
                                      Homo
                                                                           Cancer associated antigen; diagnosis;
                                                                                                                                                                                                     338 migicvtltvii 349
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                                                                                                                                                                                                                        1 LIGICVAVTVAI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-1 receptor; arthritis; retroviral vector;
                                     sapiens
                                                                                                                                                                                                                                             Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           JC,
                                                                                                                                                                                                                                                                                                                                                                      Fig 8; 60pp; English.
                                                                                                                                                                                                                                                                                            569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PITTSBURGH
                                                                                               associated antigen precursor sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-0963928.
93US-0027750.
94US-0183563.
95US-0381603.
95US-0567710.
96US-0685212.
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0924777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0630981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                        75.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robbins
                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                        Score 42;
Pred. No.
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD;
                                                                                                                                                                                                                                                                                                                                                                                                    joint, for treating arthritis in recombinant vector comprising a
                                                                      cancer;
                                                                               research;
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15;
                                                                                                                                                                                                                                                                    22;
                                                                        renal
                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                   Length 569;
                                                                        treatment;
nal cancer;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                             desired protein, a
This is useful in
                                                                        lung cancer;
                                                                                    human;
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RESULT 12
AAW43422
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Query Match
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Matches 7
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17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigen sequences and encoded polypeptides the invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and line of the cancer and cancer and cancer and cancer and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 484; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                             Binding domain; rat; syntaxin; synaptosomal-associated protein; CNS; neurotransmitter; presynaptic membrane; central nervous system; tumon neurodegenerative disease; hormonal disorder; immunological disorder
                                                                                                                                                                                                                                                                                  AAW43422 standard;
                                                                                                                                                                                        Rat syntaxin 4 protein
                                                                                                                                                                                                                                                      AAW43422;
            24-FEB-1995;
                                         02-DEC-1997.
                                                                       US5693476-A.
                                                                                                    Rattus sp.
                                                                                                                                                                                                                        27-APR-1998
                                                                                                                                                                                                                                                                                                                                                          275 liaicvsitvvl 286
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7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
97GB-0021697.
                                                                                                                                                                                                                         (first entry)
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Sahin
               9508-0393985
                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                     71.4%;
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Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB Pred. No. 17; 3; Mismatches
                                                                                                                                                                                                                                                                                       298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stockert
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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rt E;
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                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                              tumour;
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Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This amino acid sequence represents the rat syntaxin 4 protein. The invention relates to a method for identifying a compound capable of affecting the binding of a syntaxin-binding protein, e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to syntaxin. The method comprises measuring the effect of the test compound on the extent of binding between the SBP and the SBP-binding site on syntaxin. The method can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening assay for modulators of syntaxin binding - using peptide comprising binding site of syntaxin, for identifying drugs useful for treating CNS disorders, neuro-degenerative diseases, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 51-54; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cancer antigen protein sequence SEQ ID NO:1492
                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB56914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB56914 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-031743/03
Prostate cancer associated gene sequences, referred to as prostate
                             WPI; 2000-587513/55.
N-PSDB; AAF16117.
                                                                                                                                                                      08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                              WO200055174-A1
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                             vulnerary; gastrointestinal;
antibacterial; gene therapy;
                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identifying drugs capable of inhibiting or stimulating neurotransmitter release at the active zones of presynaptic membranes, which may be usefor treating CNS disorders, affective or psychotic disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STRD ) UNIV LELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-1995;
                                                                        Rosen CA,
                                                                                                 (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
                                                                                                                                            12-MAR-1999;
                                                                                                                                                                                                                                                                                                    gastrointestinal;
                                                                                                                                                                                                                                                                                                                                            neuroprotective; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 miaicvsvtvli 286
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hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LIGICVAVTVAI 12
                                                                                                                                                                                                                                                                                     infectious disease.
                                                                      Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                            99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0393985
                                                                                                                                                                                                                                                                                                  pulmonary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.48; 66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormonal or immunological disorders, tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                 cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                                                                             cardioactive; immunomodulatory; muscular; nephrotropic; antiinfective; gynaecological; neural; immune; reproductive; renal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 298;
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer antigens, useful for treatment, prevention, and diagnosis disorders such as prostate cancer - % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-small cell lung carbonic anhydrase;
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                                          Bollon AP,
                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR91951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR91951 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9602552-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung cancer specific antigen HCAVIII mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                              (CYTO-) CYTOCLONAL PHARM INC
                                                                                                                                                                                                                                                                                                           19-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liaicvsitvvl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 1928-1930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380
                                          Torczynski RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                            94US-0276919.
                                                                                                                                                                                                                                                                                                                95WO-US09145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "the phosphorylation site is recognised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- n-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; NSCLC; tumour marker; HCAVIII;
diagnosis; therapy; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.4%; 58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 1
AAR91955
Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The mature HCAVIII protein (AAR91951) was produced as a GST fusion in Escherichia coli cells transformed with the encoding cDNA (AAR15449) cloned into pGEX4T-1. It was isolated by affinity purification and thrombin cleavage. HCAVIII is a cell surface antigen which is highly specific for non-small cell lung cancer, and which shares regions of homology with human carbonic anhydrases. It can be used to produce antibodies of therapeutic or diagnostic application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 44-46; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding the lung cancer specific antigen HCAVIII useful for diagnosis and treatment of non-small cell lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-105844/11.
N-PSDB; AAT15449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91955 standard; Protein; 325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-small cell lung carbonic anhydrase; phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCAVIII phosphorylation-modified (S302G) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1996
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284 ilgicivvvsi 295
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                                                                                                                                                                          Nucleic acid encoding the lung cancer specific antigen HCAVIII useful for diagnosis and treatment of non-small cell lung cancer
                                                                                                                                                                                                                                                                                                                              19-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996
                                         A cDNA sequence (AAT15454) codes for a phosphorylation-modified form (AAR91955) of HCAVIII, a cell surface antigen which is highly specific for non-small cell lung carcinoma (NSCLO) and which has features in common with human carbonic anhydrases. The modified HCAVIII has glycine substituted for serine at position 302 of the mature protein. It is used to study the role of HCAVIII serine
                                                                                                                                                Claim 16; Page 59-60; 87pp; English.
                                                                                                                                                                                                                                                                                               (CYTO-) CYTOCLONAL PHARM INC
                                                                                                                                                                                                                                                                                                                                                          19-JUL-1995;
                                                                                                                                                                                                                           WPI; 1996-105844/11.
N-PSDB; AAT15454.
                                                                                                                                                                                                                                                                    Bollon AP,
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                              mature protein. It is used to phosphorylation in oncogenesis.
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                                                                                                                                                                                                                                                                      Torczynski RM;
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                                                                                                                                                                                                                                                                                                                                 94US-0276919
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50.0%;
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diagnosis; therapy; antibody;
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Pred. No.
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Minimum DB
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Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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US-08-685-212-2
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PCT-US95-0145A-4
US-08-776-088-4
US-08-776-088-2
US-08-776-088-4
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US-08-776-088-2
US-08-776-088-2
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US-08-776-088-6
US-08-776-088-6
US-08-776-088-7
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US-08-776-088-7
US-08-776-088-7
US-08-76-919-2
PCT-US95-09145A-2
PCT-US95-09145A-3
US-08-65-35-1
US-08-65-35-7
US-08-65-259-7
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US-08-569-853-1
US-08-569-853-1
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10.050 Million cell updates/sec
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US-07-821-716-2
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CITY: Seattle
STATE: Washing:
COUNTRY: USA
ZIP: 98101
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Appl	66,	Sequence	US-07-857-224B-66	N	265	60.7	34	5
Appl	65,	Sequence	US-07-857-224B-65	N	265	60.7	34	14
Appl	10,	Sequence	us-08-690-096-10	N	249	60.7	34	3
Appl	10,	Sequence	US-07-940-605A-10		249	60.7	34	2
Appl	44,	Sequence	US-08-789-333F-44	4	177	60.7	34	1
Appl	42,	Sequence	US-08-789-333F-42	4	173	60.7	34	0
Appl	43,	Sequence	US-08-789-333F-43	4	127	60.7	34	39
Appl	41,	Sequence	US-08-789-333F-41	4	124	60.7	34	8
Appl	14,	Sequence	US-09-133-944-14	4	51	60.7	34	37
Appl	24,	Sequence	US-09-169-015-24	4	51	60.7	34	8
Appl	14,	Sequence	US-08-789-333F-14	4	51	60.7	34	35
Appl	45,	Sequence	US-08-466-680B-45	ω	15	60.7	34	34
Appl	45,	Sequence	US-08-468-545B-45	N	15	60.7	34	3
Appl	45,	Sequence	US-08-486-348A-45	N	15	60.7	34	2
Appl	45,	Sequence	US-08-414-417B-45	_	15	60.7	34	1
Appl	45,	Sequence	US-08-467-083-45	_	15	60.7	34	õ
Appl	17,	Sequence	US-08-788-231A-17	w	465	62.5	35	9
Appl	15,	Sequence	US-08-788-231A-15	ω	462	62.5	35	8

## ALIGNMENTS

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Sequence 2, Application US/07821716 Patent No. 5319071
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APPLICANT: Dower, Steven K
APPLICANT: March, Carl J.
APPLICANT: Sims, John
APPLICANT: Urdal, David L.
                                                                                                                                                                                                              FILING DATE: 25-NOV-1987
PRIOR APPLICATION NUMBER: US 160550
FILING DATE: 25-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 258756
FILING DATE: 13-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691551
FILING DATE: 25-APR-1991
                                                                                ATTORNEY/AGENT INFORMATION:

NAME: Wight, Christopher L.

REGISTRATION NUMBER: 31,680

REFERENCE/DOCKET NUMBER: 2001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206),587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
SOFTWARE: PATION PATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                          TELEFAX: (206) 587-0606 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19920114
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 125627
FILING DATE: 25-NOV-1987
SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Soluble Interleukin-1 Receptors NUMBER OF SEQUENCES: 6
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1
    amino acids
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, MOLECULE TYPE: protein US-07-821-716-2
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US-08-381-603-2
                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-381-603-2
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Best Local Similarity
Matches 8; Conserv
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Sequence 2, Application US/08924376
Patent No. 6159464
GENERAL INFORMATION:
APPLICANT: Glorioso, Joseph C.
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                                                           US-08-924-376-2
                                                                             RESULT
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                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                             Query Match
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NAME: GOULD, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 1090
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 575-6015
TELEFAX: 626773
                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Robbins, Paul D.
TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue
TITLE OF INVENTION: Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: BAP PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (47)
TELEFAX: 866172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street Suite 3232
CITY: Philadelphia
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                                                                                                                           338 MIGICVTLTVII 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                    Local Similarity 66.
                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                          1 LIGICVAVTVAI 12
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5. 5858355
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                                                                                                                                                                                                                                                                                               linear
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66.7%;
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                                                                                                                                                                                                          Score 42; DB pred. No. 11;
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Best Local
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MEDIUM TYPE: Floppy disk
COMPOTER: IIBM PC compatible
COMPOTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street Suite 3232
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Gene Transfer For Treating a TITLE OF INVENTION: Connective Tissue of a Mammalian Host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis |
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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TELEFAX: 866172
TELEX: SEC
                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
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                                                                                                                                                                                            APPLICANT: Bandara, Geethani
TITLE OF INVENTION: Gene Transfer For Treating a
TITLE OF INVENTION: Connective Tissue of a Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/924,376 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street Suite 3232
CITY: Philadelphia
                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                         1 LIGICVAVTVAI 12
                                                                                                     STATE:
                                                                                     COUNTRY:
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8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569 amino acids
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                                                                                          USA
                                                                                                                                                                                                                                      Glorioso, Joseph C.
Evans, Christopher H.
Robbins, Paul D.
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08-MAR-1993
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66.7%;
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pred. No.
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DB 4; 11;

Length 569; Indels

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Gaps

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                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: GOULD, Jr., Lew1s F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEPHONE: (215) 575-6015
TELEX: 866172
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9402414
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Gene Transfer For TITLE OF INVENTION: a Mammalian Host NUMBER OF SEQUENCES; 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/027,750
FILLING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEFAX: (215) 575-6015
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                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: PA
COUNTRY: US
ZIP: 19103
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nes 8; Conserv
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TOPOLOGY: linear
                                TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                   TOPOLOGY:
                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Philadelphia
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1700 Market Street Suite 3232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Pittsburgh of the Commonwealth System of Higer Education WENTION: Gene Transfer For Treating a Connective Tissue of
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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protein
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Pred. No. 11;
2; Mismatches
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11;
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Query Match
Best Local Similarity
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                                                                                                                                     US-08-393-985-10
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            Sequence 10, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9608899 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 866172
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: GOULD, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-12A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: University of Pittsburgh of the Commonwealth
APPLICANT: System of Higher Education
TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue of
TITLE OF INVENTION: Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (215) 575-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                      338 MIGICVTLTVII 349
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CTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US96/08899 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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00 Market Street Suite 3232
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66.7%;
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Pred. No.
                                                                                                                                                                                                                                                                         Score 42; DB 5;
Pred. No. 11;
2; Mismatches
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11;
                                                  for Modulation
                                                                                                                                                                                                                                                                                                          Length 569;
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ADDRESSEE: STREET: 35

E: Dehlinger & Associates 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

COUNTRY:

USA

: CA RY: U: 94306

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MOLECULE TYPE: protein US-08-393-985-10
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US-08-276-919-4
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Best Local :
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Patent No. 5589579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Nelligan, Mark C.
REGISTRATION NUMBER: 36,389
REFERENCE/DOCKET NUMBER: B35792
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,919
FILING DATE:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Torczynski, Richard M.
APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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COUNTRY: US
TTD: 75270-2197
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8; Conserva
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Pred. No. 12;
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; Sequence 4, Application US/08776088 ; Patent No. 5773579

GENERAL

INFORMATION:

Torczynski, Richard M

APPLICANT:

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MOLECULE TYPE: protein US-08-276-919-4
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RESULT 10
US-08-776-088-4
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GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
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                                                                                                   Query Match
Best Local Similarity
6; Conserv
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TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Nelligan, Mark C.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 ILGICIVVVVSI 295
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TELEPHONE: 214-939-4500
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CITY: Dallas
STATE: TX
COUNTRY: US
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                                                      284 ILGICIVVVVSI 295
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                            TOPOLOGY:
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                                                                                 1 LIGICVAVTVAI 12
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75270-2197
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)GY: linear
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                                                                                                               Conservative
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50.0%;
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Pred. No.
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                                                                                                                               Score 39;
Pred. No.
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19;
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19;
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Best Local Similarity 50.0
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OPERATING SYSTEM: PC-DOS/MS-POS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,088
FILING DATE: 19-JUL-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Eugenia S. Hansen
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 10365/05011
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 18, Application US/08776088 Patent No. 5773579
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776
FILING DATE: 19-JUL-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Eugenia S. Hansen
REGISTRATION NUMBER: 31,966
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
TELEFAX: 214-981-3400
TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                              ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                       APPLICANT: Torczynski, Richard M.
APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bollon, Arthur P. TITLE OF INVENTION: Lung Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1201
CITY: Dallas
STATE: TX
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                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CITY: Dallas
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ZIP: 75270-2197
REFERENCE/DOCKET NUMBER:
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50.0%;
                                                                                                        US/08/776,088
10365/05011
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Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 325;
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Best Local Similarity
Thehes 6; Conserve
В
                           QΥ
                                           Query Match
Best Local Similarity
%** 6; Conserve
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                                                                                                                                    PCT-US95-09145A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application PC/TUS9509145A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: /JA/VIE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: John A. Harre
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 214-981-3300
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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284 ILGICIVVVVSI 295
284 ILGICIVVVVSI 295
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CITY: Dallas
STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
TYPE: a
                                                                                                                                                              LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 75270-2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 214 -981-3400
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                           1 LIGICVAVTVAI 12
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                                                         Conservative
                                                                         69.6%;
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50.0%;
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Pred. No.
                                                                         Score 39; DB 5;
Pred. No. 19;
                                                         Mismatches
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                                                                                        Length 325;
                                                         Indels
                                                         0;
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                                                         Gaps
                                                         0;
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RESULT 13 PCT-US95-09145A-18

Sequence 18, Application PC/TUS9509145A GENERAL INFORMATION:

APPLICANT: TITLE OF INVENTION: CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES:

Lung Cancer Marker 22

STREET:

ADDRESSEE:

E: RICHARDS, MEDLOCK & ANDREWS 1201 Elm Street, Suite 4500

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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-276-919-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08276919 Patent No. 5589579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: John A. Harre
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
75270-2197
7TP: 75270-2197
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,919
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Torczynski, Richard M. APPLICANT: Bollon, Arthur P. TITLE OF INVENTION: Lung Cancer Marker NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Dallas
                                            ATTORNEY/AGENT INFORMATION:
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STREET: 12.
TTTY: Dallas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LIGICVAVTVAI 12
                                                                                                                                                                                                                                          COUNTRY:
NAME: Nelligan, Mark C.
REGISTRATION NUMBER: 36,389
REFERENCE/DOCKET NUMBER: B35792
                                                                                   FILING DATE:
                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acids
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Pred. No. 19;
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SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-919-2
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Best Local Similarity ov...
6; Conservative
                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-776-088-2
 Ъ
                                                  Query Match
Best Local Similarity
Thes 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08776088 Patent No. 5773579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                  TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Torczynski, Richard M.
APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Eugenia S. Hansen
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 ILGICIVVVVSI 324
                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
313 ILGICIVVVVSI 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Dallas
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                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/776,088 FILING DATE: 19-JUL-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                              1 LIGICVAVTVAI 12
                                                                                                                                                                                                      ENGTH:
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                                                                  Conservative
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                                                                                69.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                         10365/05011
                                                                  score 39; DB
Pred. No. 21;
4; Mismatches
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                                                                                               DB 1; Length 354;
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                                                                         Gaps
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Search completed: November 13, 2001, 14:26:50

Job time: 36 sec

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Query
Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
BLOSUM62
Gapop 10.0 ,
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56
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pir2: *
pir3: *
pir4: *
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F28559
F42518
F42518
C727160
C727160
C73726
A36187
A36187
F48213
F148213
F1493080
F132331
F149670729
F24616
F370749
F370681
E69874
F30881
F105874
A30412
C844462
C844462
C844462
G70713
HAIG1
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probable peptide t
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hemoglobin alpha c
bplK protein - Bor
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Al4L protein - var
interleukin-1 rece
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syntaxin-4 - human
syntaxin 4 - rat
       conserved hypothet probable murx prot low affinity trypt tryptophan transpo hypothetical prote hemoglobin alpha-I
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Al3L protein - vac
                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                        Al3L protein - var
PD6-glycoprote
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Qy 1 LIGICVAVTVAI 12	Query Match 100.0%; Score 56; DB 2; Length Best Local Similarity 100.0%; Pred. No. 0.0083; Matches 12; Conservative 0; Mismatches 0; Inde	RESULT 2 TR8555 TR8555 hypothetical protein A14L - variola major virus C. Species: variola major virus C. Species: variola major virus C. Accession: T2855 C. Accessio	Oy 1 LIGICVAVTVAI 12             Db 7 LIGICVAVTVAI 18	Query Match 100.0%; Score 56; DB 2; Length Best Local Similarity 100.0%; Pred. No. 0.0083; Matches 12; Conservative 0; Mismatches 0; Inde	RESULT 1 E36849 A13L protein - variola virus (strain India-1967) C; Species: variola virus C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C;Accession: E36849 R;Blinov, V.M. submitted to GenBank, November 1992 A;Reference number: A36859 A;Accession: E36849 A;Accession: E36849 A;Accession: E36849 A;Accession: E36849 A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49058.1; PI	ALIGNMENTS	30 36 64.3 364 2 G86340 31 36 64.3 366 2 T27257 32 36 64.3 422 2 S52578 33 36 64.3 422 2 T46332 34 36 64.3 457 2 T46332 35 64.3 1472 2 B54774 36 64.3 1529 2 A59189 37 36 64.3 1529 2 A59189 38 35 62.5 134 2 I46090 39 35 62.5 134 2 I46091 40 35 62.5 134 2 I46091 41 35 62.5 141 2 A61485 42 35 62.5 184 2 B72168 43 35 62.5 184 2 B72168 44 35 62.5 184 2 B72168 45 35 62.5 184 2 T28578
	ngth 68; Indels 0; Gaps 0;	<pre>xt_change 21-Jul-2000 terback, T.R.; Knight, J.C.; Au regions of variola smallpox vir 60865.1; PID:g439035</pre>		ngth 68; Indels 0; Gaps 0;	change 23-Mar-2001		protein F2D10.35 f hypothetical prote serine/threonine-s hypothetical prote hypothetical prote ATP binding casset ATP-binding casset ATP-binding casset aTP-binding casset aTP-binding casset penome polyprotein ubiquinolcytochr ubiquinolcytochr ubiquinolcytochr ubiquinolcytochr ubiquinol-membrane benoglobin alpha c probable membrane A37R protein - var A36R protein - var BR protein - vario

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A13L protein - vaccinia virus (strain Copenhagen)
C; Species: vaccinia virus
A; Note: host Homo sapiens (man)
C; Date: 09 Nov-1990 #sequence_revision 09-Nov-1990 #1
C; Accession: F42518
R; Johnson, G.P.
submilted to GenBank, June 1990
A; Reference number: A33172
A; Accession: F42518
A; Status: preliminary
A; Status: preliminary
A14L protein - variola minor virus (strain Garcia-1966)
A14L protein - variola minor virus
C;Species: variola minor virus
C;Accession: C72165
C;Accession: C72165
A;Bescription: Analysis of the complete coding sequence of DNA of alastrim variola minor
A;Beference number: A72150
A;Accession: C72165
A;Status: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecules: 1-68 <SHC>
A;Cross-references: GB:Y16780; NID:95830555; PIDN:CAB54717.1; PID:e1542673; PID:95830678
A;Experimental source: strain Garcia-1966
C;Gene: A14L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-70 <JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Variety: strain Ankara

G; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change

C; Accession: T37400

C; Accession: T37400

R; Antoine, G.; Schelflinger, F.; Falkner, F.G.; Dorner, F.

R; Antoine, G.; Schelflinger, F.; Falkner, F.G.; Dorner, F.

R; Antoine, G.; Schelflinger, F.; Falkner, F.G.; Dorner, F.

R; Antoine, G.; Schelflinger, F.; Falkner, F.G.; Dorner, F.

A; Reference number: Z20877

A; Reference number: Z20877

A; Recession: T37400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structural protein p8 - vaccinia virus (strain Ankara)
C;Species: vaccinia virus
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A; Residues: 1-70 <ANT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U94848; PIDN:AAB96464.1
A;Experimental source: strain Ankara
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Best Local Similarity
Matches 12; Conserv
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Matches
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illarity 100.
Conservative
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Pred. No. 0.0085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; pred. No.
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(.)Species: Homo sapiens (man)
(.)Species: Homo sapiens (man)
(.)Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 29-Sep-1999
(.)Accession: A36187; S06928
(.)Accession: A36187; S06928
Proc. Natl. Acad. Sci. U.S.A. 86, 8946-8950, 1989
Proc. Natl. Acad. Sci. U.S.A. 86, 8946-8950, 1989
A;Title: Cloning the interleukin 1 receptor from human T cells.
A;Reference number: A36187; MUID:90046906
A;Accession: A36187; MUID:90046906
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A;Cross-references: GDB:125254; OMIM:147810
A;Map position: 2q12-2q12
C;Superfamily: interleukin-1 receptor type I
C;Keywords: cytokine receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Chua, A.O.; Gubler, U.
R;Chua, A.O.; Gubler, U.
Nucleic Acids Res. 17, 10114, 1989
A;Title: Sequence of the cDNA for the human
A;Reference number: $06928; MUID:90098789
A;Accession: $06928
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A; Residues: 1-569 <SIM>
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A; Residues: 1-569 <CHU>
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                                                                                                                                                                                                         C;Accession: C64637

C;Accession: C64637

R;Tomb, J.F., White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R;Tomb, J.F., White, O.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McK peterson, S.; Loftus, B.; Richardson, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997

N.; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A; Jitle: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID:97394467

A; Accession: C64637
                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid ABC transporter, permease protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 20-Aug-1999
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Best Local
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                                                                                      A;Residues: 1-237 <TOM>
A;Cross-references: GB:AE000603; GB:AE000511;
C;Superfamily: histidine permease protein M
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                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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Best Local 9
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8; Conserv
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pred. No. 0.039;
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Pred. No.
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                                                                                                                                    NID:g2314075; PIDN:AAD07984.1;
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Length 68;
Indels
 0;
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U

J.M.; March, C.J.;

fibroblast type interleukin-1 receptor

EMBL:X16896; NID:g33800; PIDN:CAA34773.1; PID:g33801

Length 569; Indels 0; Gaps 0;

PID:g231

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syntaxin - human
C;Speckes: Homo saplens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Sep-1999
C;Accession: I38517
R;Li, H.; Hodge, D.R.; Pei, G.K.; Seth, A.
Gene 143, 303-304, 1994
A;Title: Isolation and sequence analysis of the human syntaxin-encoding gene A;Reference number: I38517; MUID:94266173
A;Accession: I38517
syntaxin 4 - rat
(;Species: Rattus norvegicus (Norway rat)
(;Species: Rattus norvegicus (Norway rat)
(;Date: 06:Jan-1995 #sequence_revision 06-Jan-1995 #text_change;
(;Accession: E48213

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-297 <JAC>
A;Cross-references: EMBL:X85784; NID:g758104; PIDN:CAA59769.1; PID:g758105
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E48213
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C;Superfamily: syntaxin
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R;Jagadish, M.N.; Fernandez, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         syntaxin-4 - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999
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Matches 7
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7; Conserv
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Pred. No. 14;
3; Mismatches
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Pred. No.
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12;
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <BEN>
A;Cross references: GB:L20821; NID:g349320;
C;Superfamily: syntaxin
                                                                                                                                                                    A:Title: Sequence and analysis of the 60 kb conjugative, A:Reference number: 222314
A:Accession: T43080
A:Status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C41G6.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999 C;Accession: T19880
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-114 <DOU>
                                                                                                                                                                                                                                         C;Accession: T43080
R;Dougherty, B.A.; Hill, C.; Weidman, J.F.;
Mol. Microbiol. 29, 1029-1038, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 5
A: Introns: 203/2;
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A; Residues: 1-573 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z19191
C; Superfamily: Staphylococcus aureus transfer
                  A;Genome: plasmid pMRC01
A;Note: ORF00008
                                                                             A; Experimental source: strain
                                                                                 A;Cross-references: EMBL:AE001272; PIDN:AAC55994.1
A;Experimental source: strain DPC3147
                                                                                                                                                                                                                                                                                                 C;Species: Lactococcus lactis
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: clone C41G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z81047; PIDN:CAB02826.1; GSPDB:GN00023; CESP:C41G6.2
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                                                                                                                                                                                                                                                                                                                                           hypothetical protein - Lactococcus lactis plasmid pMRC01
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275 MIAICVSVTVLI 286
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Pred. No.
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Pred. No. 44;
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14;
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complex protein trsB
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Conservative

4.

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67.9%; 50.0%;

Score 38; DB Pred. No. 14;

2;

Length 114;

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-207 <ROH>
A;Cross-references: EMBL;AF025451; PIDN:AAB71204.1; GSPDB:GN00020; CESP:C24H12.8
A;Experimental source: Strain Bristol N2; clone C24H12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T32331
R;Rohlfing, T.; Wohldmann, P.; Biewald, T.
R;Rohlfing, T.; Wohldmann, P.; Biewald, T.
Submitted to the EMBL Data Library, September 1997
submitted to the sequence of C. elegans cosmid C24H12.
A;Reference number: Z21151
A;Accession: T32331
A;Accession: T32331
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32331
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                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20263314

A;Accession: B83705

A;Catus: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04161.1; GSPDB:GNOC A;Experimental source: strain C-125
C;Genetics:
                                                                                                              RESULT 15
D70729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphonates transport system (permease) BH0442 [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000 C;Accession: B83705
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A; Introns: 27/3; 53/2; 138/2
probable peptide transport system permease - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: D70729 C;Accession: D70729 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; G
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B83705
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C;Superfamily: phnE protein
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7; Conserv
  Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
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Pred. No. 23;
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Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987
A; Accession: D70729
                                                                                                                                                                                                                                                                    A;Cross-references: GB:Z77164; GB:AL123456; NID:g3261615; PIDN:CAB01002.1; PID:g32616
A;Experimental source: strain H37Rv
                                                                                                                                                                                                         A;Gene: oppC
C;Superfamily: oligopeptide permease protein oppB
                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-291 <COL>
  В
                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
86 LIGVCVAV
                                              1 LIGICVAV 8
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87.5%;
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Search completed: November 13, 2001, 14:28:19 Job time: 125 sec

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Result
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Maximum Match 100%
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Copyright (c) 1993 - 2000 Com
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CYB_ANOCU
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CYB_CHORA
YJR5_YEAST
CYB_GLOSA
CYB_TADBR
VA33_VABP
CYB_RHIFE
Y4TQ_RHISN
Y4TQ_RHISN
TORK
YATQ_RHISN
CYB_TANCA
CYB_PITSU
ERB2_MOUSE
                                                                                                                              HBA_BRATR
MRAY_MYCTU
TNAB_ECOLI
HBA1_IGUIG
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Query Match
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Matches 12; Conserv

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swiss-prof entry is copyright. The Swiss Institute of Bioin bioinformatics Institute by non-profit institutions as sized and this statement is not relies requires a license agreement and an email to license@isb-sib.cl  x69198; CAAA49058.1; -  £22579; AAA60865.1; -  £36849; E36849.  E36849; E36849.	PubMe PubMe Osito 1 L., 1 vall	IL.  Us.  IDNA viruses, no RNA s  us.  10255;  OM N.A.  OM N.A.  OSCARIOLATE IND3  OSCARIOLA and Vaccinia v  mechanisms.";  319:80-83(1993).	STANDARD; 1. 28, Creal 1. 28, Last 1. 33, Last	247 406 540 604 634 953 1210 1210 1254 1255 1255
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Viruses; dsDNA '
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MEDLINE-91021027; PubMed=2219722;
Goebel S.J., Johnson G.P., Perkus
Paoletti E.;
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SEQUENCE
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P14778;
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01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR (IL-
(P80) (ANTIGEN CD121A).
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Eukaryota; Metazoa; (
Mammalia; Eutheria; l
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  SEQUENCE FROM
TISSUE=T-cell;
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                                                                                                                                                            TISSUE=Liver;
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MEDLINE=90046906; PubMed=2530587; Sims J.E., Acres R.B., Grubin C.E., March C.J., Dower S.K.; March C.J., Dower S.K.; Teceptor "Cloning the interleukin 1 receptor proc. Natl. Acad. Sci. U.S.A. 86:89
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MEDLINE=97215904; PubMed=9062194;
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 SEQUENCE
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A36187; A36187.
IITB; 04-FEB-98.
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Query Match Best Local

Similarity

75.0%; 66.7%;

Score 42; Pred. No.

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Length

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STX4_HUMAN

ID STX4_H
AC 012846
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Q12846; Q15525;
Q1-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Lens epithelium;
Rae J.L., Shepard A.R.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: POTENTIALLY INVOLVED IN DOCKING OF SYNAPTIC NAT PRESYNAPTIC ACTIVE ZONES.
-I- SIMILARITY: BELONGS TO THE SYNTAXIN/EPIMORPHIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-96332494; PubMed-8760387;
Jagadish M.N., Fernandez C.S., Hewi
Gough K.H., Grusovin J., Verkuylen
Frenkel M.J., Ward C.W.;
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=94266173; PubMed=8206394;
Li H., Hodge D.R., Pei G.K., Seth A.;
"Isolation and sequence analysis of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNIFAL
STX4A OR STX4.
HOMO Sapiens (Human).
HOMO Sapiens (Homan).
Horta; Metazoa; Chordata; Hortmates;
Pfam; PF00804; Syntaxin; 1.
PROSITE; PS00914; SYNTAXIN;
Neurotransmitter transport;
DOMAIN 43 163
DOMAIN 199 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Peripheral blood neutrophils; Nabokina S., Lazo P.A., Mollinedo F. Submitted (JUL-1997) to the EMBL/Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Insulin-responsive tissues contain the core (synaptosomal-associated protein 25) A and B syntaxin 4 and synaptobrevins 1 and 2."; Biochem. J. 317:945-954(1996).
                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1998 (Rel. 36, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                    InterPro;
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01-NOV-1997
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CONFLICT
CONFLICT
SEQUENCE
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30-MAY-2000
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SEQUENCE
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HSSP;
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                                                                                                                                                                                                                                                                                                                                   "Characterization of Munc-18c and syntaxin-4 in PRESYMAPTIC ACTIVE ZONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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DOMAIN
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                                                                                                                                                                        Neurotransmitter transport;
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                                                                                                                                                                                         Pfam; PF00804; Syntaxin;
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                                                                                                                                                                                                                                                                                                                                                                                     James D.E.;
                                                                                                                                                                                                                                                                                                                                                                                             Tellam J.T., Macaulay S.L., McIntosh S.,
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
NCBI_TaxID=10116;
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30-MAY-2000 (Re
SYNTAXIN 4.
STX4A OR STX4.
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MEDLINE-93386759; PubMed-7690687;

Mennett M.K., Garcia-Arraras J.E., Elferink L.A., Pettennett M.K., Garcia-Arraras J.E., Elferink L.A., Pettenneng A.M., Hazuka C.D., Scheller R.H.;

"The syntaxin family of vesicular transport receptors cell 74.863-873(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q08850;
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SEQUENCE
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-i- SIMILARITY: BELONGS TO THE SYNTAXIN/EPIMORPHIN FAMILY
                                                                                                                                                                                                                                                                                                                   CARC_HUMAN STANDAKU;
CARC_TOMAN
CASTO;
CASTO;
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurotransmitter transport;
DOMAIN 38 163
DOMAIN 199 223
TRANSMEM 275 295
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-98301622; PubMed=9636197;

MURECI O., Sahin U., Vollmar E., Siemer S., Gottert E., Seitz G.,

Parkkila A.K., Shah G.N., Grubb J.H., Pfreundschuh M., Sly W.S.;

Parkkila A.K., Shah G.N., Grubb J.H., expression, and

"Human carbonic anhydrase XII: cDNA cloning, expression, and

"Human carbonic anhydrase XII: cDNA cloning, expression, and

chromosomal localization of a carbonic anhydrase gene that is

chromosomal some renal cell cancers.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                      NCBI_TaxID=9606;
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275 MIAICVSVTVLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00804;
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8; Conserv
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PS00914; SYNTAXI
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Rodentia;
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Sciurognathi; Muridae;
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9E854270DFB3CB96 CRC64;
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Stanbridge E.J., Kerman M.I.;

Stanbridge E.J., Kerma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=98445416; PubMed=9770531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long use by non-this statement is not removed. Entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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MIM; 603263;
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Q10623; Q50698; 34, Created)
Q1-QCT-1996 (Rel. 34, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PUTATIVE PEPTIDE TRANSPORT PERMEASE PROTEIN R
RV1282C OR MTCY373.01C OR MTCY3H3.01.
     STRAIN=H37RV;
MEDLINE=98295987;
Cole S.T., Brosch
                                                                                                                                      Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                          Mycobacterium tuberculosis.
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2; EUK_CO2_ANHYDRASE; ?
2; FUK_Tane; Signal.
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           PubMed=9634230;
R., Parkhill J.,
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N-LINKED (GLCNAC...)
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01-FEB-1995 (I
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                                                                                                                "Molecular analysis of the anaerobic succinate degradation pathway Clostridium kluyveri.";
J. Bacteriol. 178:871-880(1996).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-i- SIMILARITY: BELONGS TO THE UPF0077 (PECM) FAMILY.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium kluyveri.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                  MEDLINE-96146540; PubMed-8550525; Soehling B., Gottschalk G.;
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                                                                                                                                                                                                                                                                                                                            STRAIN-DSM 555;
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TE; PS00402; BPD_TRANSP_INN_MEMBR; 1
Transport; Peptide
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291 AA;
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L 33.5 KDA PROTEIN IN CAT1 5'REGION (ORFY).
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a clear the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                      "Gene content and organization of a the extremely thermophilic archaeon, Genome 43:116-136(2000).

i- FUNCTION: INVOLVED IN PROTEIN FXI
                                                                                                                                                                                                                                                                                                                                                                                                                 Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C., Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D., Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She O., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., St Jean A., Sensen C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-DSM 1617 / P2;
STRAIN-20165948; PubMed-10701121;
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
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                                                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus solfataricus
Archaea; Crenarchaeota;
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                                       EMBL; Y18930; CAB57608.1;
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                                                                                                                                                                                                                                                FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PIBY FORMING PART OF A CHANNEL.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
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netical protein; Transmembrane
                                                                                 an email to license@isb-sib.ch).
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01-JAN-1990 (Rel. 13, Cr

01-JAN-1990 (Rel. 13, La

01-OCT-2000 (Rel. 40, La

HEMOGLOBIN ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                        **Rieinschmidt T., Marz J., Braunitzer G.;

*Rheinschmidt T., Marz J., Braunitzer G.;

*The primary structure of pale-throated three-toed sloth (BradyF

*The primary structure of pale-throated three-toed sloth (BradyF

**Tridactylus, Xenarthra) hemoglobin.";

**tridactylus, Xenarthra) hemoglobin.";

**tridactylus, Xenarthra) hemoglobin.";

**BIOL Chem. Hoppe-Seyler 370:303-308(1989).

**Indiactylus, Xenarthra 170:308 To XYGEN TRANSPORT FROM THE LUNG TO THE

**JANUARITY: BELONGS TO THE GLOBIN FAMILY.

**JANUARITY: BELONGS TO THE GLOBIN FAMILY.
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Budaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Edentata; Bradypodidae; Bradypus.
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                                                                                                                                                                                   METAL
SEQUENCE
                                                                                                                                                                                                                                                                  Interpro; IPR000971; -.
Interpro; IPR002338; -.
Pfam; PF00042; globin; 1.
PRINTS; PR00612; ALPHAHAEM.
PROSITE; PS01033; GLOBIN; 1
  100
                                       1 LIGICVAVTVAI 12
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LLGHCVLVTLAL 111
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8; Conserv
                                                                                                                                                                                                                                               Oxygen transport; Respiratory
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                                                                              Similarity 58...
7; Conservative
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nilarity 72.7%;
Conservative
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87
141
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13, Last seq
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58.3%;
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                                                                                     Score 37; DB
Pred. No. 14;
3; Mismatches
                                                                                       ω,.
                                                                                                                                                                                      iratory protein; Erythrocyte.
IRON (HEME DISTAL LIGAND).
IRON (HEME PROXIMAL LIGAND).; 2808540F975F9435 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    three-toed sloth (Bradypus
                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 469
                                                                                              2;
                                                                                                                                 Length 141;
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RESULT

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RX COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
RC "Deciphering the biology of Mycobacterium tuberculosis from the
"Deciphering the biology of Mycobacterium tuberculosis from the
"Deciphering the biology of Mycobacterium tuberculosis In THE
Complete 93:537-544(1998).

C. -: FUNCTION: FIRST STEP OF THE LIPID CYCLE REACTIONS IN THE
BIOSYNTHESIS OF THE CELL WALL PEPTIOOGLYCAN (BY SIMILARITY).

C. -: CATALYTIC ACTIVITY: UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMYL-L-
C. -: CATALYTIC ACTIVITY: UDP-N-ACETYLMURAMOYL-L-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL-D-ALANYL
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006221;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
PHOSPHO-ACETYLMURAMOYL-PENTAPEPTIDE TRANSFERASE
(UDD-MURAMC-PENTAPEPTIDE PHOSPHOTRANSFERASE).

(UDD-MURAMC-PENTAPEPTIDE PHOSPHOTRANSFERASE).

WRAY OR MURX OR RV2156C OR MTCY270.12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; pF00953; Glycos_transf_4; pR0SITE; PS01347; MRAY_1; 1. pR0SITE; PS01348; MRAY_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TubercuList; Rv2156c;
InterPro; IPR000715; -
Pfam; Pr00953; Glycos_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     TRANSMEM
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SEQUENCE
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TRANSMEM
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                                                                           y Match
Local
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 4. MRAY
                                                                                                                                                   SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIPHOSPHOUNDECAPRENOL.
1 LIGICVAVTVAI
                                                        Similarity 66.8; Conservative
                                                                                                                                                                354
37713
                                                                                66.1%;
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POTENTIAL.
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                                                                                    Score 37; DB pred. No. 30;
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                                                                   Mismatches
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tent is in no
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J. Bacteriol. 147:795(1981).

J. Bacteriol. 147:787-796(1981).

J. Bacteriol. 147:787-796(1981).

J. Bacteriol. 147:787-796(1981).

J. Bacteriol. 147:787-796(1981).

CYTOPLASMIC MEMBRANE, PLAY A ROLE:IN TRANSPORTING TRYPTOPHAN CYTOPLASMIC MEMBRANE. PLAY A ROLE.IN TRANSPORTING TRYPTOPHAN CYTOPLASMIC MEMBRANE PROTEIN. INNER MEMBRANE.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.

-!- INDUCTION: BY TRYPTOPHAN. IS SUBJECT TO CATABOLIC REPRESSION.

-!- SIMILARITY: BELONGS TO THE MTR / TNAB / TYRO PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNAB_ECOLI
P23173;
01-NOV-1991
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                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12 / MG1655; MEDLINE-93315143; Pubmed=7686882; Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; Burland Brown and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication."; Genomics 16:551-561(1993).
                                                                                                                                                                                          EMBL; K00032; AAA24677.1; -. EMBL; M59914; AAA62792.1; -. EMBL; L10328; AAA62060.1; -. EMBL; AE000448; AAC76732.1; -.
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A new family of integral membrane proteins involved aromatic amino acids in Escherichia coll.";

J. Bacteriol. 173:3231-3234(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia
Bacteria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOW AFFINITY
TNAB OR TRPP
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01-NOV-1997
                                                                                                           Transport;
                                                                                                                        PRINTS; PR00166; AROAAPRMEASE.
PROSITE; PS00594; AROMATIC_AA_PERMEASE_1; 1.
                                                                                                                                                    InterPro;
                                                                                                                                                                 EcoGene; EG11006; tnaB.
                                                                                                                                                                             PIR; A39412; A39412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deeley M.C., Yanofsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82007678; PubMed=6268608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of the structural gene for tryptophanase
                                                                                                                                                    IPR002091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria;
                                                                                                             Amino-acid
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(Rel. 35, Last annota
TRYPTOPHAN PERMEASE.
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35, Last annotation
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212
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                                                                                                             transport;
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                                                                                                             Inner membrane
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Best Local :
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Q34462;
15-JUL-1999 (Rel. 38, Cree
15-JUL-1999 (Rel. 38, Last
30-MAY-2000 (Rel. 39, Last
CYTOCHROME B (FRAGMENT).
MTCYB OR COB OR CYTB.
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P18974;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence up
01-JUN-1994 (Rel. 29, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89207099; PubMed=3242545;
Rueckhagel K.P., Braunitzer G., Wiesner H.;
"Hemoglobins of reptiles. The primary structures of the alpha
beta I-chains of common iguana (Iguana iguana) hemoglobin.";
Biol. Chem. Hoppe-Seyler 369:1143-1150(1988).
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Iguana iguana (Common iguana).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ranianeanria: Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
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  STRAIN-LSUMZ
Sudman P.D.,
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Mammalia; Eutheria;
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HSSP; P01922; 1FDH.
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Chiroptera; Microchiroptera; Moloss:
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54.5%;
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IRON (HEME PROXIMAL LIGAND).
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Best Local Similarity
Matches 6; Conserv
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J. Mammal. 75:365-377(1994).

-i. FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX II OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.

COUPLED TO ATP SYNTHESIS.

-i. COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY POCHAIN TO THE DECRETARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BOUND TO THE PROTEIN.

FOUND TO THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.

FOUND TO THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME B FAMILY.
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Pfam; PF00033; cytochrome_b_N; 1.

PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

PROSITE; PS00193; CYTOCHROME_B_QO; PARTIAL.

PROSITE; PS00193; CYTOCHROME_B_QO; PARTIAL.

PROSITE; PS00193; CYTOCHROME_B_QO; PARTIAL.
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66.1 502 10 Q9SP14 Q9SP14 G9SP14 G9SP14 G9SP15 G9SP15 G9SP15 G9SP15 G9SP15 G6.1 552 5 P91765 m F71787 G6.1 559 2 P71787 G71787 G7178 G71787 G7178 G71787 G7178 G71787 G7178 G7178 G7178 G7178 G7178 G7178 G7178 G7178 G7178		025112	N	111		36	31
66.1 502 10 Q9SP14 66.1 510 10 Q9SP15 66.1 510 10 Q9SP15 66.1 552 5 P91765 P91765 m 66.1 559 2 P71787 66.1 599 2 P71787 66.1 944 4 Q14697 66.1 966 4 Q9P0X0 Q9P0X0 b 66.1 966 11 008794 66.1 973 3 Q9Y7Q7 66.1 973 4 Q81890 Q9Y7Q7 66.1 2233 14 Q81890 Q9J7166 66.1 2233 14 Q9J7D6 Q9J7166		Q9J7D0	14	2233		37	30
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66.1 502 10 Q9SP14 alo 66.1 510 10 Q9SP15 929 66.1 552 5 P91765 P91765 myzu 66.1 559 2 P71787 P71787 myco 66.1 944 4 Q14697 Q14697 homo 66.1 966 4 Q9P0X0 Q9P0X0 homo 66.1 966 11 008794 008794 mus		Q9Y7Q7	w	973		37	27
66.1 502 10 Q9sp14 alo 66.1 510 10 Q9sp15 sysp15 sysp15 sysp165 myzu 66.1 552 5 p91765 p91765 myzu 66.1 599 2 P71787 p71787 myco 66.1 594 4 Q14697 Q14697 homo 66.1 966 4 Q9P0X0 Q9p0X0 homo		008794	11	966		37	26
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66.1 502 10 Q9SP14 Q9SP14 G9SP15 G9SP15 G9SP15 66.1 552 5 P91765 P91765 66.1 599 2 P71787 P71787		Q14697	4	944		37	24
66.1 502 10 098P14 098p14 66.1 510 10 098P15 098p15 66.1 552 5 P91765 P91765		P71787	N	599		37	23
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                              Q9JF84;
Q9JF84;
Q1-OCT-2000;
01-OCT-2000;
01-OCT-2000;
TALL;
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NCBI_TaxID=126794;
[11
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057225;
01-JUN-1998
01-JUN-1998
01-MAR-2001
Vaccinia virus (strain Tian Tan).
Viruses; dsDNA viruses, no RNA stage;
Orthopoxvirus.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ANKARA;
Antoine G., Scheiflinger F., Falkner F.G., Dorner F.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databas:
EMBL; U94848; AAB96464.1; -.
SEQUENCE 70 AA; 7644 MW; C5E59815B7BF7955 CRC64;
                                                                                                                                                                                                                                                                                                                                                           STRUCTURAL PROTEIN P8. MVA124L.
                                                                                                                                                                                                                                                                                                                                    Vaccinia virus (strain Ankara).
Viruses; dsDNA viruses, no RNA stage;
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7 LIGICVAVTVAI 18
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                                          Created)
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Pred. No.
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             Poxviridae; Chordopoxvirinae;
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SEQUENCE FROM N.A.

STRAIN-TIAN TAN;

Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang

Jin Q., Yu W.H., Yuan J.S., Ma X.J.;

Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;

"Complete genomic sequence of vaccinia virus (Tian Tan s

"Complete genomic sequence of vaccinia virus (Tian Tan s

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1998) to the Zenzelinia virus

"Complete genomic sequence of vaccinia virus

"Complete genomic Seq
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Q89163;
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-variola minor virus; STRAIN-GARCIA-1966; Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F., Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F., Bassung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Pars Esposito J.J., Sosnovtsev S.; Bassung S., Sosnovtsev S.; Squence of DNA of alastrim "Analysis of the complete coding sequence of DNA of alastrim minor virus strain Garcia-1966."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; X16780; CAB54717.1; -. EMBL; X16780; CAB54717.1; -. EMBL; X16780; CAB54717.1; -. SEQUENCE 68 AA; 7569 MW; 32BB87801903315E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SPECIES-Variola virus; STRAIN-GARCIA-1966;
SPECIES-Variola virus; STRAIN-GARCIA-1966;
Shchelkunov S.N., Totmenin A.V., Sosnovtsev S.V.,
Resenchuk S.M., Blinov V.M., Sandakhchiev L.S.;
Resenchuk S.M., Blinov V.M., Sandakhchiev L.S.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ data
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Viruses; dsDNA viruses, no
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01-JAN-1998
01-JAN-1998
01-JUN-2000
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                                                          01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2000 (TrEMBLrel. 14,
AMINO ACID ABC TRANSPORTER,
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      Helicobacter
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      pylori (Campylobacter pylori)
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RNA stage; Poxviridae;
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Pred. No.
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No.
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MEDLINE-97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.D., Dougherty B.A
Teleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
Kington M.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                         Q9P8G5
Q9P8G5;
01-OCT-2000
01-OCT-2000
01-MAR-2001
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Nature 388:539-547(1997).
Nature AE000603; AAD07984.1;
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Hypothetical protein.
SEQUENCE 237 AA; 26351 MW;
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NCBI_TaxID=210;
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                                                                                                                                                                                      InterPro;
Pfam; PF0(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                       Gupta G.D., Heath B.I.;
"Neurospora crassa putative
submitted (MAY-2000) to the
EMBL; AF262964; AAF72704.1;
                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota;
Sordariales; Sordariaceae; Nei
                                                                                                                                                                                                                                                                                                                                                           PUTATIVE
 017654
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                      Neurospora
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                                                             295 LGICVATIVVI 305
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ILGLCIAVFVAL
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                                                                                                              Similarity 7; Conserv
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IPR000727;
                                                                                                                                                                                                                                                                                                                                       crassa.
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AA; 52175 MW;
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16,
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Last annotation update)
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Pred.
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                                                                                                                              Score 39;
Pred. No.
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                                                                                                                                                                                                                                                                                                                            Pezizomycotina;
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      PRT;
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databases.
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Dougherty B.A.,
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Science 282:2012-2018(1998).
EMBL; Z81047; CAB602826.1; -.
EMBL; Z83116; CAB60294.1; -.
EMBL; Z81047; CAB60294.1; JOIN
SEQUENCE 573 AA; 66076 MW;
                                                                                                                                       Q9E207;
01-MAR-2001
01-MAR-2001
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01-JAN-1998
01-JAN-1998
01-MAY-2000
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson J.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Sounders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
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Caenorhabditis elegans.
Cukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                             Q9E207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
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Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam "Complete Sequence of the Simian Varicella Virus Genome."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                           01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
MEMBRANE PROTEIN.
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                                                                         Cercopithecine herpesvirus 7.
Viruses; dsDNA viruses, no RNA stac
Alphaherpesvirinae; Varicellovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                                       SEQUENCE FROM N.A.
                                                              NCBI_TaxID=35245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the
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8; Conservative
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13,
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MW; 096FF19E591851A8
                                                                                     RNA stage; Herpesviridae;
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Last sequence update)
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Last sequence update)
Last annotation update)
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Pred. No. 88;
4; Mismatches
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017160;
01-JAN-1998 (TrEMBLrel. (
01-JAN-1998 (TrEMBLrel. (
01-MAR-2001 (TrEMBLrel. 1
C24H12.8 PROTEIN.
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01-NOV-1998
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087210;
        Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L. Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
                                                                                                                                                                                                                                                                                                                                                                            "Sequence and analysis of the 60 kb plasmid pMRC01 from Lactococcus lact Mol. Microbiol 29:1029-1038(1998).
EMBL; AE001272; AAC55994.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF275348; AAG27247.1; SEQUENCE 87 AA; 9693 MW;
                                               Wilson R., Ai
Bonfield J.,
                                                                    STRAIN-BRISTOL N2; MEDLINE-94150718; PubMed-7906398;
                                                                                                                     Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                      C24H12.8
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                                                                                        SEQUENCE FROM N.A.
                                                                                                           NCBI_TaxID=6239;
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LVGVCVALFIII
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 Rifken L.,
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                                                                                                                      oda; Chromadorea; Caenorhabditis.
                                                                                                                                                                                                                                                                                                      Score 38; DB Pred. No. 26; 4; Mismatches
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is DPC3147.";
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 Α.,
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EMBL; AF025451; AAB71204.1; -

R InterPro; IPRO01810; -

Pfam; PF00646; F-box; 1.

PROSTIE; PS50181; FBOX; 1.

SEQUENCE 207 AA
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
STRAIN-BRISTO
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Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
elegans.";
elegans.";
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STRAIN-C-125 / JCM 9153;
Takami H , Nakasone K , Takak
Takami H , Nakasone K , Takak
Submitted (MAR-2000) to the E
EMBL; AP001508; BAB04161.1;
InterPro , IPR000515;
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Q9KEN7;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUNCEPHONATES TRANSPORT SYSTEM (PERMEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
[2]
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STRAIN-BRISTOL N2;
062368 PRELIMINARY;
062368;
01-AUG-1998 (TrEMBLrel. 0
01-AUG-1998 (TrEMBLrel. 0
01-JAN-1999 (TrEMBLrel. C
T06G6.2 PROTEIN.
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Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus halodurans
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                                                                                                                                                                                                                                                                                                                    IVGICLSIVLAI
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BPD_transp; 1. AA; 28649 MW;
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24415 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
63
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P.,
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                                       07, Created)
07, Last sequence update)
09, Last annotation update)
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e EMBL/GenBank/DDBJ
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB pred. No. 55; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6;
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44;
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RESULT
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Anderson K.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Carxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Cardner A., Green P., Hawkins T., Hillier L., Johnston L.,
Gardner A., Green P., Hawkins T., Hillier L., Jer M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Latster N., Latreille P.,
Allightning J., Lloyd C., Momurray A., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Aparsons J., Smith A., Sonnhammer E., Staden R., Sulston J.,
Aparsons J., Smith A., Sonnhammer E., Staden R., Sulston J.,
Aparsons J., Smith A., Sonnhammer E., Staden R., Sulston J.,
And Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Thierry Meinstock L., Wilkinson-Sproat J., Wohldman P.;
A Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
BY T., Bis87; CAB64702.1;
BY T. BY T., CAB64
                                                                                                                                                 RX MEDLINE-20437337; PubMed-10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
"Opportunistic pathogen.";
RI Nature 406:959-964 (2000).
REMBL; AEO04550, AAG04592.1; -.
RW Hypothetical protein.
W Hypothetical protein.
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Q914D5;
Q914A5;
Q91AP5;
Q91AP5;
Q1-MAR-2001 (TrEMBLrel. 16, Cr
Q1-MAR-2001 (TrEMBLrel. 16, La
T Q1-MAR-2001 (TrEMBLrel. 16, La
T Q1-MAR-2001 (TrEMBLrel. 16, La
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Best Local
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                      Query Match
Best Local
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NCBI_TaxID=6239;
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Caenorhabditis elegans.
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Bacteria; Proteobacteria;
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6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
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Score
Pred.
3; Mis
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45;
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                                                                                  Length 135;
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Matches

Similarity 54.6 6; Conservative

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If "Independent Expression and Iron Regulation of the 1sp Gene in 
"Independent Expression and Iron Regulation of the 1sp Gene in 
"Independent Expression and Iron Regulation of the 1sp Gene in 
"Independent Expression and Iron Regulation of the 1sp Gene in 
"Independent Expression and Iron Regulation of the 1sp Gene in 
"Independent Expression and Iron Regulation of the 1sp Gene in 
"Independent Expression and Iron Regulation of the 1sp Gene in 
"Independent Expression and Iron Regulation of the 1sp Gene in 
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"Independent Expression and Iron Regulation of the 1sp Gene in 
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"Independent Expression and Iron Regulation of the 1sp Gene in 
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"Independent Expression and Iron Regulation of the 1sp Gene in 
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"Independent Expression and Iron Regulation of the Iron Regulation of
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Best Local
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01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
PUTATIVE GTG
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequenc
01-MAR-2001 (TrEMBLrel. 16, Last annotat
LIPOPROTEIN SIGNAL PEPTIDASE (EC 3.4.23.
PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE
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                              STRAIN-BP536; PubMed-8821935; MEDLINE-96419162; PubMed-8821935; Allen A.G., Maskell D.J.; The identification, cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01252; Peptidase_A8; 1. PRINTS; PR00781; LIPOSIGPTASE. PR05ITE; PS00855; SPASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF201388; AAF19640.1; ...
InterPro; IPR001872; ...
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STRAIN-ATCC13883;
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Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RF47;
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    Bordetella
                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                               Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q45385
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                                                                                                                                                                                                                               NCBI_TaxID-520;
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease; Hydrolase; Lipoprotein; Transmembrane.
166 AA; 18410 MW; 474857EDCD0C85EF CRC64;
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      lipopolysaccharide
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77.88;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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i mutagenesis
biosynthesis
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3.4.23.36) (PROLIPOPROTEIN SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 166;
a genetic locus
Bordetella
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RX KEDLINE-98044033; PubMed=9384377;
RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Fritz C., Fujita M., Fujita Y., Funas S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Funas S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Purnelle B., Parwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Taxeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
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Best Local
STRAIN-168;
Kunst F., Ogasawara N., Y
Submitted (NOV-1997) to t
EMBL; 299110; CAB13008.1;
SEQUENCE 218 AA; 23745
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O31603;
O1-JAN-1998
O1-JAN-1998
O1-NOV-1998
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Mol. Microbiol. 19:37-52(1996).
EMBL; X90711; CAA62254.1; -.
SEQUENCE 193 AA; 21015 MW;
                                                                                                                                                                                                                                                                  Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Dan
"The complete genome sequence of the gram-positive bacteri
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                                                                                                                                                          SEQUENCE
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      Z99110; CAB13008.1;
NCE 218 AA; 23745
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6; Conserv
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                                                                                                                                                       FROM N.A.
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Pred. No.
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         EA254C8E95A90700 CRC64;
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61;
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Best Local Similarity 58.35; Fred. No. 68;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
LIGICVATVAL 12

pb 135 VIGLUSVEVII 146

Search completed: November 13, 2001, 14:34:01

Job Line: 427 sec
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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           A_Geneseq_0601:*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*

6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*

7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*

8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*

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       DВ
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AAP10416
AAP50222
AAP60127
AAP61403
AAP60576
AAP70922
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                                          AAP90630
AAR15713
AAR26819
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13.377 Million cell updates/sec
Novel decapeptide
LuteInising hormon
Sequence of lutein
Peptide #1 with ho
LH releasing hormo
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Gonadotropin relea
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AAP10411
ID AAP1
           \begin{array}{c} \mathsf{D} \times \mathsf{X} \times \mathsf{D} \times \mathsf{X} \times \mathsf{D} \times \mathsf{X} \times \mathsf{X} \times \mathsf{D} \times \mathsf{X} \times \mathsf{X} \times \mathsf{D} \times \mathsf{X} \times \mathsf{
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHRH; Follicle Stimulating Factor; FSH; acne; hirsutism; dysmennorhea; precocious puberty; endometriosis; prostate cancer; benign prostate hypertrophy; mammary tumour.
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                                                                                                                                                                                                                                  21-SEP-1979;
                                                                                                                                                                                                                                                                                                        23-FEB-1983;
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Minimum DB Maximum DB

Searched:

Sequence:

Run on:

Database

Luteinising Hormon	AAB68693	22	10	100.0	63
Mammalian luteinis	AAB73047	22	10	100.0	63
GnRH monomer	AAB71947	22	10		63
Luteinising hormo	AAY55061	21	10	•	63
	AAY58136	21	10	•	63
Luteinising	AAY68566	21	10		63
LHRH target	AAY91197	21	10	100.0	63
Luteinising hormon	AAY79054	21	10	•	63
Mammalian releasin	AAY82376	21	10	•	63
Gonadotrophin-Rele	AAY88576	21	10	•	63
Gonadotrophin rele	AAB06261	21	10	•	63
Luteinising hormon	AAB03590	21	10		63
Amino acid sequenc	AAB08103	21	10		63
=	AAY96084	21	10		63
	AAB20777	21	10	•	63
Gonadotropin relea	AAB20863	21	10	100.0	63
ש	AAB15362	21	10	•	63
Gonadorelin peptid	AAB10930	21	10	•	63
	AAW83360	20	10	•	63
Hormone doma	AAW84278	20	10		63
Lutei	AAW96765	20	10	100.0	63
LHRH peptid	AAW94890	20	10		63
Amino acid seque	AAY03856	20	10	100.0	63
Non-crosslinked p	AAY31067	20	10		63
	AAY31176	20	10		63
Neutrophil-activ	AAY50229	20.	10		63
Œ	AAW76373	19	10		63
5	AAW04612	18	10		63
	ŧл	18	10	•	63
	520	17	10	•	63
Luteinising hormon	AAW65201	17	10	100.0	63
	515	16	10	•	63
dotropin rel	83	16	10	100.0	63
LHRH peptide. Syn	AAR91197	16	10	100.0	63

## ALIGNMENTS

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LH-RH, liberating factor for LH and FSH, and its agonists compsn.
                                    WPI; 1981-23409D/14 (23409D).
                                                                     (ROUS ) ROUSSEL UCLAF.
                                                                                                        79FR-0023545
                                                                                                                                           83BE-0468932
                                                                                                                                                                                                                                                                 /note= "pyroglutamic
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Result No.

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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A composition is claimed containing LHRH or its analogues. The composition is used to treat prostate adenocarcinoma, benign hypertrophy of the prostate, endometriosis, dysmenorrhea, hirsutism hormone-dependent mammary tumours, for treatment or prevention of precocious puberry, delaying the onset of puberty and for treating acne. The compositions may also contain antiandrogens. See also AAP10412-P10418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - used to treat prostate adenocarcinoma, benign hypertrophy the prostate, hirsutism, acne, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1(a); Page 15; 27pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      LHRH; Follicle Stimulating Factor; FSH; acne; hirsutism; dysmennorhaa; precocious puberty; endometriosis; prostate cancer; benign prostate hypertrophy; mammary tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP10416 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luteinising Hormone Releasing Hormone analogue #5.
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A composition is claimed containing LHRH or its analogues. The composition is used to treat prostate adenocarcinoma, benign hypertrophy of the prostate, endometriosis, dysmenorrhea, hirsutism hormone-dependent mammary tumours, for treatment or prevention of precocious puberty, delaying the onset of puberty and for treating
                                                                                        LH-RH, liberating factor for LH and FSH, used to treat prostate adenocarcinoma, the prostate, hirsutism, acne, etc.
                                                                                                                                                                                                                                  19-MAR-1981
                                                                   Claim 1(f); Page 16; 27pp; French.
                                                                                                                                       WPI; 1981-23409D/14 (23409D).
                                                                                                                                                                                    21-SEP-1979;
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                                                                                                                                                                                                                                                                                                                              'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                'label=
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                                                                                                                                                                                                                                                                                                                                                   "pyroglutamic acid"
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                                                                                                                                                                                                                                                                                                                    "N-alpha-methyl-Leu"
                                                                                                                                                                                                                                                                                                                                                                 OTHER
                                                                                                                                                                                                                                                                                   is Pro-NH-C2H5"
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Pred. No.
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                                                                                                            and its agonists compsn-
benign hypertrophy of
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                                 hirsutism,
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Matches 10; Conserv
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AC AAP6
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30-AUG-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gonadotrophin
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                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1985
                                                                                                                                                                                                    The claimed peptide antagonists inhibit the release of gonadotrophins and/or steroids. They are antagonistic to GnRH, inhibit ovulation, and may cause resorption of a fertilised egg if administered shortly after absorption. The peptides also have utility in male contraception, and in treatment of precoscious puberty, hormone dependent neoplasia, dysmenorrhoea and endometriosis.
                                                                                                                                                                                                                                                                                                        New GnRH antagonist peptide(s) - useful as inhibitors of gonadotropin(s) and/or steroid(s) for contraceptive use.
                                                                                                                                                                                                                                                                                  Disclosure; Page 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                          WPI; 1985-136434/23
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                                                                                                                                                                               Sequence
AAP60127
                       AAP60127 standard; Peptide;
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 {\tt AAP10411-P10418}\,.
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                                                                                                                           Conservative
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85US-0771517.
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Pred.
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Pred. No. 0.00012;
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide gonadotropin releasing hormone antagonists - esp. as contraceptives, for treating early puberty, hormone-dependent neoplasms etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1986-299774/46
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Prepn. of gonadotropin liberating hormone and analogues - by multistage rapid peptide synthesis in soln. without isolating
                                                                                                                                                                                                                                                                             08-MAY-1984;
                                                                                                                                                                                                                                                                                                                                         08-MAY-1984;
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Pred. No. 0.00012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analogue; peptide synthesis;
fertility;
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Best Local Similarity 100
Matches 10; Conservative
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Best Local :
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                                                                                                                                 Sequence
                                                                                                                                                            Peptide inhibits the release of lutenising hormone releasing hormone. See also AAP60575.
                                                                                                                                                                                                      Disclosure; Page 990; 5pp; Japanese.
                                                                                                                                                                                                                                                                                                                                      23-AUG-1984;
                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-1986.
                                                                                                                                                                                                                                                                                                                                                                                                                          JP61210098-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lutenising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel decapeptide with LHRH inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-0CT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                 Deca:peptide - inhibits LH-RH hormone release activity
                                                                                                                                                                                                                                                              WPI; 1986-321434/49.
                                                                                                                                                                                                                                                                                           (TULA-) ADMIN TULANE EDUCAT.
(TULA ) TULANE E FUND ADMINISTRA.
                                                                                                                                                                                                                                                                                                                                                                 23-AUG-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intermediates
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1 ehwsyglrpg 10
1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hormone releasing hormone activity.
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Pred. No.
                                                       Score 63; DB /, Pred. No. 0.00012;
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                                                                                    Length 10;
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AAP70922 standard; peptide;

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Page 4
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHRH; contraception; precocious puberty; endometriosis; breast tumours; prostate tumours; ectopic tumours; meno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luteinising hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                 Orally active luteinising hormone-releasing hormone peptide analogues - have keto:methylene or hydroxy:ethylene in place amide between proline(9) and glycine(10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                   This luteinising hormone releasing hormone (LHRH) agonist has either a ketomethylene or dihydroketomethylene gp. replacing the amide linkage between residues 9 and 10 in LHRH. This results in an increase in oral activity. It is useful for eg male and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Almquist RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US4705778-A
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; page 4; 17pp; English.
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                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                              an increase in oral activity. It is useful for eg male and female contraception, treatment of precocious puberty and endometriosis and treatment of breast and prostate tumours.
                                                                                                                                                                                                                                                                                                    See also AAP70923-27.
                                                                                          AAP90630;
         Luteinizing hormone releasing hormone (LHRH); LHRH antagonist; 19-nor-progestational agent; female gynaecological disorders.
                                            Sequence of
                                                                   14-JUN-1989
                                                                                                                AAP90630 standard;
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|ehwsyglrpg
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                                                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative 0
                                            luteinizing hormone releasing hormone (LHRH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olsen CM;
                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "other= ketomethylene(Gly), dihydroketo-
    methylene(Gly)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               releasing
                                                                                                                  protein;
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Pred. No. 0.00012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ectopic tumours; menopause.
                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                               Gaps
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AAR15713
ID AAR1
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                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                Analogues (I) of the sequence pref. have amino acid (AA) substitutions at posns. 2 (his is replaced by a D-AA) and 6 (gly is replaced by a D-AA). A therapeutically effective amt. of such an antagonist is contained in a pharmaceutical compson. alongside a menopausal-symtom-alleviating amt. of a 19-nor progestational agent (II) (pref. both in single formulation). A pref. administered nasally in dosages of 0.01-1 mg/kg/ day for (II) and 0.02-0.07 mg/kg/day for (II). May be used for inhibition of ovulation, and treatment of eg endometriosis, breast cancer, polycistic ovarrian disease, or precocious puberty in female mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP301850-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SYNT ) SYNTEX (USA) INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           steroid producn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsn. comprising LHRH-antagonist and 19-nor progestational for treating female gynaecological disorders based on gonads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1989-033720/05
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                   AAR15713;
                                                                                                                                                                                                                                                                                       AAR15713
                                                                                                                                                                                  synthetic.
                                                                                                                                                                                                                                              24-JAN-1992
                                                                                                                                                      Modified-site
                                                                                                                                                                                                                          Peptide #1
                                                                                                                                                                                                        luliberin.
                     22-APR-1991;
                                                             WO9116343-A.
                                                                                                    Modified-site
                                                                                                                         Modified-site
                                         31-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           1 EHWSYGLRPG 10
                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                       ehwsyglrpg 10
                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                        standard; Protein; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                             with homology to LHRH.
                                                                                                                                                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87US-0080518
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                      91WO-FR00332
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                   /note=
                                                                                                                                             /label=
                                                                                  /note=
                                                                                             /label= OTHER
                                                                                                                'label= Hyp
                                                                                  "amidated"
                                                                                                                                   "pyroGlu"
                                                                                                                                               OTHER
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                            Score 63; Pred. No.
                                                                                                                                                                                                                                                                                           AΑ
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 10;
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23-APR-1990;

90FR-0005147

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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The C-terminal residue (Gly-CO-NH2) can be replaced by ethylamide. This peptide and fragments of it (i.e. amino acids 4-10, 5-10, 6-10 and 7-10) are agonists and antagonists of LHRH. They are useful for treating e.g. precoclous or delayed puberty, psychiatric disorders esp. those of the libido or sexual aggression, etc. In addition they are useful for functional exploration of the hypothalamus-hypophyseal are useful for functional exploration of the hypothalamus-hypophyseal axis and for radioimunological or biological assay (of LH, FSH and
       New deca:peptide luteinising hormone-releasing hormone antagonists - for treating precocious puberty, hormone dependent tumours, endometritis, cystic diseases; also as contraceptive
                                                                                                                                                                                                                                                                                                                                        Luteinising hormone; LHRH; hypothalamic; antiovulatory; tumours; antineoplastic; precocious puberty; ovulation; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR26819 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 steroid levels) in biological fluids and biopsy samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide homologous with luteinising hormone-releasing hormone used to treat gynaecological conditions, cancer of gonads and sec. sexual organs, psychiatric conditions and in assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRM ) INSERM INST NAT SANTE
                                                                                                                                      30-JAN-1991;
                                                                                                                                                               29-JAN-1992;
                                                                                                                                                                                        20-AUG-1992
                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                               LH releasing
                                                                                                           (TULA ) TULANE EDUCATIONAL FUND.
                                                                                                                                                                                                                WO9213883-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EHWSYGLRPG 10
||||||||||
1 ehwsyglrpg 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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                                                                                  Juhasz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                               hormone antagonists
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                     91US-0647786.
                                                                                                                                                               92WO-US00776
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                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                /label- pGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
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                                                                                   Schally AV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63; DB 12;
Pred. No. 0.00012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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RESULT 1
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Best Local S
Matches 10
                                                                                                                                                                                                                                   (LADD/) LADD A I
(WANG/) WANG C I
(ZAMB/) ZAMB T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     puberty, hormone dependent tumours, e.g. malignant and benign prostate tumours, e.g. secondary amenorihoea, endometriosis and ovarian and mammary cystic diseases. The peptide is also useful for regulating ovulation e.g. as precoital or postcoital contraceptives, for synchronising oestrus in livestock and for improving the "rhythm" method. It is also useful for regulating the human menopausal gonadotropin, follicle stimulating and LH levels during premenopausal and postmenopausal periods. As it suppresses the spermatogenesis and testosterone levels in males, it may be of potential use for male contraception.
Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxic T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which possesses high antiovulatory and antineoplastic activity, is free of anaphylactoid side effects and is believed to be free of endematogenic effects. The peptide may be used to treat precocious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 1; 43pp;
                                                                                                                                                                        WPI; 1994-357910/44.
                                                                                                                                                                                                                                                                                                27-APR-1993;
14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                        WO9425060-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                androgen-dependent carcinoma; antitumour; infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helper T cell epitope; universal immune stimulator; invasin; hapten;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHRH hapten for attachment to universal immune stimulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR62689;
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                                                                                                                                                                                                                                                                                                                                           28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                           Immunogenic luteinising hormone releasing hormone peptide(s)
that suppress LHRH activity in males and females
                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          decapeptides is an antagonistic analogue of hypothalamic LHRH
                                                                                             Page 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHRH;
                                                                                                                                                                                                   Wang CY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.
nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
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94US-0229275.
                                                                                                                                                                                                                                                                                                                                           94WO-US04832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 luteinising
                                                                                           213pp; English.
                                                                                                                         activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                                                        Zamb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hormone releasing hormone;
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Pred. No. 0.00012;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
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cc a heterogeneous population expressing diverse HLA phenotypes, and (8) cc an adjuvant peptide sequence from the invasin protein of versinia. cc spacer amino acid sequences (e.g. Gly-Gly) can be provided between the components in the hapten is LHRH, then optionally the invasin domain components. When the hapten is LHRH, then optionally the invasin domain components equence represents an LHRH hapten which can be the present sequence represents an LHRH hapten which can be cattached to the stimulator to provide a potent vaccine for attached to the stimulator to provide a potent vaccine for creating e.g. prostatic hyperplasia, androgen-dependent carcinoma, constructions tumours, recurrent functional ovarian cysts, (severe) conduction of infertility.
RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHRH peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-1996
                                                                                                                                                                                                                                                                                                                  CA1335403-C
                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                         luteinising hormone releasing hormone; follicle stimulating; FSH;
                                                                                                                                                                                   Gauthier
                                                                                                                                                                                                                                       06-MAY-1988;
                                                                                                                                                                                                                                                              06-MAY-1988;
                                                                                                                                                                                                                                                                                       25-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
A new method is provided for preparing a decapeptide of formula pGlu-His-Trp-Ser-Tyr-Xaa-Leu-Arg-Pro-Gly-NH2, in which a protected nonapeptide corresponding to the N-terminal of the peptide is first prepared on a benzhydrylamine resin, the Pro residue being attached
                                                                                                    Prepn. of luteinising hormone and follicle stimulating hormone releasing peptide(s) - by cleaving a protected nona-peptide reby photolysis to remove the support, coupling with glycinamide
                                                                                                                                                                                                           (BOEH ) BIO-MEGA/BOEHRINGER INGELHEIM RES
                                                                 Claim 1; ; 18pp;
                                                                                          deprotecting
                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EHWSYGLRPG
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                                                                                                                                                           1995-179260/24
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10; Conser
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                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.
                                                                                                                                                                                                                                                                                                                                                                     "pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                              "Gly-NH2"
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. 0.00012;
ches 0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-OCT-1992;
14-DEC-1990;
14-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gonadotropin releasing hormone; GnRH; motility disorder; functional bowel disease; leuprolide acetate; luteinising hormone; progesterone; relaxin; autonomic nervous system; drug delivery; the irritable bowel syndrome; diabetes; scleroderma; Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gonadotropin releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR86845 standard;
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This sequence represents naturally occuring gonadotropin releasing hormone (GnRH). Analogues of GnRH are represented by AAR86846-56.

Motility disorders, including functional bowel disease, can be treated by the administration of one of the GnRH analogues shown here (e.g. by the administration of one of the GnRH analogue inhibiting leuprolide acetate). This is due to the GnRH analogue inhibiting production of reproductive hormones such as luteinising hormone, progesterone and relaxin. Motility disorders are caused from progesterone and relaxin motility disorders are caused from abnormalities of the autonomic nervous system. Due to this, the GnRH abnormalities of the autonomic nervous system.
                                                                                                                                                                                                                                                                                        Treating motility disorders associated with systemic lupus erythematosus - by admin. of gonadotropin releasing hormon analogue, to control nausea, vomiting, abdominal pain etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-1995
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                                                                                                                                                                                                                                      Disclosure; Column 3; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-263259/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mathias JR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MATH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATHIAS J R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0965675.
90US-0626402.
91US-0744977.
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Pred. No.
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Best Local Similarity

Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analogues may also exert effects on the autonomic nervous system. The GORH analogues are administered by injection (which may be intavenous, subcutaneous or intramuscular), or by a drug delivery system. The drug delivery system can comprise a drug implant with timed release, a nasal spray or an injection of a long-lasting depo form. This method is used to alleviate symptoms such as nausea, vomiting, abdominal pain and altered bowel habits. The sequences can be used to treat motility disorders in a wide variety of other diseases including irritable bowel syndrome, diabetes, scleroderma and Parkinson's disease.
                                                                                                                                           8 Different forms of GnRH (given in AAR75152-59) have previously been isolated from vertebrate species. A precursor for an additional form of GnRH, (Ser8)-GnRH (AAR75151), has now been
                                                                                                                                                                                                                         New gonadotropin releasing hormone preprohormone DNA - used to develop prods. for regulation of reproductive function and diagnosis of reproductive capacity and disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gonadotropin releasing hormone; GnRH; gonadoliberin; reproduction; transgenic animal; transgenic fish; transgenic fowl.
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                                                                                                                                                                                                Disclosure; Fig.1a; 85pp; English.
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                                                                                                       Sequence
                                                                                                                                                                                                                                                                                 WPI; 1995-185526/24.
                                                                                                                                                                                                                                                                                                          Adelman JP,
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1 EHWSYGLRPG 10
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10; Conservative
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Pred. No. 0.00012;
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Pred. No. 0.00012;
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16-SEP-1992;
07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradykinin; N-benzylglycine; agonist; receptor study; antagonist; achiral; analgesic; luteinising hormone-releasing hormone; LHRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gonadoliberin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW65201 standard; peptide; 10
                                                                                           Sequence
                                                                                                                   peptide by the replacement of selected amino acids with achiral amino acids. The present sequence represents a
                                                                                                                                 The invention relates to the obtaining of a potent agonist or antagonist peptide by the replacement of selected amino acids with synthetic
                                                                                                                                                               Disclosure; Columns 11-12; 15pp; English.
                                                                                                                                                                                 New bradykinin analogues contg. N-benzyl-glycine -bradykinin agonists or antagonists, useful e.g. as
                                                                                                                                                                                                                  WPI; 1996-299898/30.
                                                                                                                                                                                                                                     Mitchell AR,
                                                                                                                                                                                                                                                                                                                   07-NOV-1994;
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1 EHWSYGLRPG
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                                         10;
                                                     Similarity
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                                          Conservative
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                                                                                                                                                                                                                                                         CALIFORNIA
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92US-0945664.
94US-0335202.
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                                                                                                               hormone
                                                    100.0%;
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                                                                                                               (LHRH).
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Pred. No.
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                                          Mismatches
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                                                  DB 17;
0.00012;
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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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   DB
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US-07-690-983D-3
US-07-690-983D-3
US-07-690-983D-3
US-08-343-883-1
US-08-08-341-219-11
US-08-488-888-22
US-08-446-692-1
US-08-488-351A-1
US-08-488-351A-1
US-08-488-351A-1
US-08-488-351A-1
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US-08-124-491-18
US-08-124-491-18
US-08-912-118-13
US-08-912-118-13
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1 EHWSYGLRPG

Query Matc Best Local Matches	US-07-714-540-9  US-07-714-540-9  Sequence 9, Applicati Patent No. 5262521  GENERAL INFORMATION: APPLICANT: Alnqui APPLICANT: TOll, TITLE OF INVENTION ITITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: Irel STREET: 545 Mid CITY: Menlo Par STATE: Californ COUNTRY: USA ZIP: 94025  COMPUTER READABLE MEDIUM TYPE: F1. COMPUTER: IBM P OPERATING SYSTEM SOFTWARE: Paten CURRENT APPLICATION APPLICATION NUM APPLICATION NUM REFERENCE/DOCKET TELEPHONE: 415-32 TELEPHONE: 415-32 TELENGTH: 10 amin LENGTH: 10 amin LENGTH: 10 amin INFORMATION FOR SEO SEQUENCE: TYPE: pr US-07-714-540-9  US-07-714-540-9		4 4 4 4 4 4 3 3 3 3 3 3 3 3 3 3 3 3 3 3
.ch 100. 1 Similarity 100. 10; Conservative	QULT 1 QUAT 14-540-9 equence 9, Application US/07714s atent No. 5262521 general INFORMATION: APPLICANT: Almquist, Ronald of APPLICANT: Toll, Lawrence TITLE OF INVENTION: ISOLATED TITLE OF INVENTION: ENZYME AN NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: ADDRESSEE: Irell & Manella STREET: 545 Middlefield Roc CITY: Menlo park STATE: California COUNTRY: USA ZIP: 94025 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: Patentin Release CURENTY APPLICATION DATA: APPLICATION NUMBER: US/07/. FILING DATE: 19910607 CLASSIFICATION INFORMATION: NAME: Reed, Dianne E. REGISTRATION INFORMATION: NAME: Reed, Dianne E. REGISTRATION INFORMATION: TELEPAN: 415-327-7250 TELEFAX: 415-327-7250 TELEFAX: 415-327-7250 TELEFAX: 415-327-7250 TELEFAX: 10 amino acids TYPE: AMINO ACID STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein 07-714-540-9		63 100.0 63 100.0 63 100.0 63 100.0 63 100.0 63 100.0 63 100.0 63 100.0 63 100.0 63 100.0
100.0% 100.0% tive	on:  ON:  ON:  ON:  Quist, Ronald G   Lawrence   ION: ENZYME ANI ION: STATE  Compatible Floppy disk # PC DOS/MS: LentIn Release   FION DATA: TION DATA: TION DATA: UNFORMATION: 19910607 INFORMATION: 19910607 INFORMATION: 11910607 INFORMATION: 11910607 INFORMATION: 15-327-7250 15-327-2951 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		114 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
; Score 63; DB 1; Length ; Pred. No. 7e-05; 0; Mismatches 0; Indel	ATRIAL PEPTIDE-DEGRADING NOVEL COMPOUNDS USEFUL 1d, Suite 200 #1.0, Version #1.25 #1.0, Version #1.25	ALIGNMENTS	US-08-302-915-2 US-07-690-983D-22 US-07-690-983D-26 US-07-690-983D-30 US-07-690-983D-16 US-07-690-983D-16 US-07-690-983D-16 US-07-690-983D-20 US-08-48-351A-12 US-08-488-351A-17 US-08-488-351A-17 US-08-488-351A-17 US-08-488-351A-17
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Gaps	INHIBITORS 1		22, Appl 22, Appl 24, App 30, App 16, App 28, App 28, App 12, App 12, App 11, App 11, App 12, App 29, App
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US-07-690-983D-2
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                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                    Sequence 32, Application US/07690983D Patent No. 5403586
                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                             APPLICANT: RUSSELL-JONES, Gregory J.
APPLICANT: STEWART, Andrew G.
APPLICANT: STEWART, CON G.
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: FUSION PROTEINS NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/AU90/00373
FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 1
FILING DATE: 25-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
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COMPUTER READABLE FORM
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                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                           1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
Gy: unknown
                  20007-5109
                                             Washington, D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEWART, Andrew G
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                                                                  3000 K Street, N.W.
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US-07-690-983D-32
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Best Local Similarity
Matches 10; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn RelacTRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 16786/148 CHAC TELECOMMUNICATION INFORMATION: TELEPHONE: (202)572-5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00373
APPLICATION NUMBER: PCT/AU90/00373
AFILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bonneau, Michel B.
TITLE OF INVENTION: wethod for improving the organoleptic
TITLE OF INVENTION: qualities of the meat from uncastrated male domestic
TITLE OF INVENTION: animals, vaccines which are usable in this method, ne
TITLE OF INVENTION: peptide, in particular for producing these vaccines.
                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 25-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
COMPUTER: II
                                                      FILING DATE: 17-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,495
FILING DATE: 09-NOV-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Larson and Taylor
STREET: 727 Twenty-Third Street, South
CITY: Arilington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                        APPLICATION NUMBER: US/08/343,883 FILING DATE: 17-NOV-1994
                     APPLICATION NUMBER: FR 9 FILING DATE: 01-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Application US/08343883 5573767
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amino acid
GY: linear
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Roulet, Claude J.M.
Chouvet, Claire D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          animals, vaccines which are usable in this method, new peptide, in particular for producing these vaccines...
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                                            FR 9102513
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Pred. No. 7e-05;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids

APPLICATION NUMBER: FR 9 FILING DATE: 10-DEC-1991

FR 9115289

TYPE: amino acid

TOPOLOGY:

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                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application Patent No. 5578477 GENERAL INFORMATION:
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Best Local Similarity
Matches 10; Conserv
                                                                   ZIP: 2007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/000,931
FILING DATE: 05-JAN-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                APPLICANT: Tamanoi Dr., Fuyuhiko
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: INHIBITORS OF PROTEIN FARNESYLTRANSFER,
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1
OTHER INFORMATION: /le
OTHER INFORMATION: /nc
PUBLICATION INFORMATION:
                         ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EATURE:
                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide LOCATION: 10
                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
REFERENCE/DOCKET NUMBER: 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EHWSYGLRPG 10
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Schally, A. V.
Structure of the porcine LH- and
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Baba, Y.
G. Nair, R. M.
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          64098/102/ARDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63;
Pred. No.
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-000-931-5
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Best Local Similarity
"hehes 10; Conserve
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NAME/KEY: Modified-site LOCATION: 10 CORTER INFORMATION: /note US-08-428-488-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5624894
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Appris
                                                                                                                                                                                                                              TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: BR
TITLE OF INVENTION: PE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                       OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Baumeister, Mary K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                          FEATURE:
NAME/KEY:
                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/O FILING DATE: 27-APR-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                              NAME: Baumeister, Mary Katherine REGISTRATION NUMBER: 26,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria
STATE: Virginia
                                                                                                           LOCATION:
                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EHWSYGLRPG 10
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                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BODOR, Nicholas S.
                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRAIN-ENHANCED DELIVERY OF NEUROACTIVE PEPTIDES BY SEQUENTIAL METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 63; DB 1; 100.0%; Pred. No. 7e-05;
                /note= "Position 10 = Gly-NH2."
                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/428,488
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                                                                                        "Position 1 =
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I.OCATION: 10
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-341-219-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rivier, J.
APPLICANT: Powell, J.
APPLICANT: Sherwood, N.
APPLICANT: Gothilf, Y.
APPLICANT: Gothilf, Y.
APPLICANT: INVENTION: Compounds and P.
TITLE OF INVENTION: Reproduction in
NUMBER OF SECUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
   Best Loc
Matches
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CORUZZÍ, LAURA A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 83:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEPHONE: (212) 790-9990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: COruzzi,, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: N V
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: un
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                            LOCATION: 1
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0
FILING DATE: 05-DEC-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                            NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
100.0%; milarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      10 amino acids
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                                                                                                                                                                                                                                                                                                                       NO
                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                               peptide
NO
                                                                                                                                                                                                                                                                                                                                                                                      not relevant
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                                                                                                                                                                                                             /product= "OTHER"
/label= Glu1
/note= "=pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/341,219
                                                                                                         /product= "OTHER"
/label= Gly10
/note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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           0;
         Score 63; DB 1;
Pred. No. 7e-05;
Mismatches
                                              DB 1;
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                                            Length 10;
           Indels
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                  0,:
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                  Gaps
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                    0;
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US-08-453-588-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 22, Application US/08453588 ; Patent No. 5684145
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
US-08-453-588-22
                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                   US-08-591-917-1
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                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                              Sequence 1, Application US/08591917 Patent No. 5707964
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/078,66
ETLING DATE: 16-JUN-1993
ETLING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: MATY E. GOTMLEY
REGISTRATION UNMBER: 34,409
REGISTRATION: 18FORMATION:
TELECOMMUNICATION 18FORMATION:
                    GENERAL INFORMATION:

APPLICANT: Nett, Torrance M
APPLICANT: Nett, Torrance M
APPLICANT: Olode, Leonard Michael
APPLICANT: Glode, Leonard Michael
TITLE OF INVENTION: A METHOD FOR TREATING CANCER
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
ADDRESSEE: Sheridan Ross & McIntosh
CITY: Denver
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anna van der Zee, Irma Marianne van APPLICANT: Willem Pietter Martin Hoekstra, APPLICANT: Josephus Theodorus Gielen.
TITLE OF INVENTION: Carrier system against GRRH NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: AKZO NO. 5684145el Patent Department STREET: 1300 Piccard Drive, Suite 206 CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 30-MAI CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                         1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                          1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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            Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anna van der Zee, Irma Marianne van Die,
                                                                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glu at position 1 is pyroglutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (301) 258-5200
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16-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                  score 63; DB 1;
Pred. No. 7e-05;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                       0.
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Indels

0;

Gaps

COMPUTER READABLE FORM:

COUNTRY: U ZIP: 80203

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US-08-446-692-1
                                                        COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692

FILING DATE: 7-JUN-1995

CLASSIFETCATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: MARIA C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745

TELEPHONE: (212)415-8745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application Patent No. 5759551
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/591
FILING DATE: 26-JAN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KOVARÍK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2730
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR EGO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 100.0%; Score 63; DB 1; Length 10; Local Similarity 100.0%; Pred. No. 7e-05; hes 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 10154-0053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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RESULT 12 US-08-694-865-18

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Best Local Similarity
Watches 10; Conserve
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US-08-796-598-6
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                                                             Matches
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                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                 TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,598
FILING DATE: 07-FEB-1997
CLASSITICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PATTERSON, DALE H.
APPLICANT: TARR, GEORGE E.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: SY TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: FLYNN Esq., Kerry A
REGISTRATION NUMBER: 33,69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: High
CITY: Boston
                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Patent Administrator - Testa, Hurwitz & ADDRESSEE: Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EHWSYGLRPG 10
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1 EHWSYGLRPG 10
                            1 EHWSYGLRPG 10
                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6, Application US/08796598
5. 5827659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                            10;
                                                                                                                                                                                                 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High Street Tower, 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                     ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                           100.0%; Score 63; DB 2; 100.0%; Pred. No. 7e-05;
                                                                                                                                                                                                                                                                                                                                33,693
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Pred. No. 7e-05;
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                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 10;
                                                                                        Length 10;
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                                                             Indels
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; OTHER INFORMATION: /note= "This position is pyroGlu." US-08-694-865-18
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US-08-488-351A-1
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Best Local Similarity
Transparents 10; Conser
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                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08488351A Patent No. 5843446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: POTTER, ANDREW A. APPLICANT: MANNS, JOHN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                          TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 285 HAM.
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                     APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
COUNTRY: US
ZIP: 10154-0053
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10 amino acids
TYPE: amino acid
TYPE: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site LOCATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                           CITY: New York
                                                                                                      ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; score 63; DB 2; Length 10; 100.0%; Pred. No. 7e-05; Indels
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3ER: 9001-0016.22
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, MOLECULE TYPE: peptide US-08-488-351A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08480494B Patent No. 5843901 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATIA C.H. Lin 29,323
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATA:
CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: 1992
APPLICATION APPR-1992
APPLICATION APPR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 7-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patent
                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 7-CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Roeske, Roger W.
TITLE OF INVENTION: LHRH Antagonist Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-007
TELECOMMUNICATION INFORMATION:
                                                   ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                           STREET: 60 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                        APPLICATION NUMBER: US/08/480,494B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 amino acids
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                             60 State Street, Suite 510
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Pred. No. 7e-05;
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COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,175A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,137
REFERENCE/DOCKET NUMBER: SP-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-447-175A-6
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TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 63; DB 2; Length 10 Best Local Similarity 100.0%; Pred. No. 7e-05; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08447175A Patent No. 5869240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: PATTERSON, DALE H.

APPLICANT: PATTERSON, DALE H.

TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
TITLE OF INVENTION: SPECTROMETRY.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: High
CITY: Boston
STATE: MA
1 EHWSYGLRPG 10
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1 EHWSYGLRPG 10
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ADDRESSEE: Thibeault, LLP
STREET: High Street Tower, 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EHWSYGLRPG 10
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                                                                                     100.0%; Score 63; DB 2; Length 10; ilarity 100.0%; Pred. No. 7e-05; Conservative 0; Mismatches 0; Indels
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                                                                                         Gaps
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Search completed: November 13, 2001, 14:26:49 Job time: 35 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
         PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match Length DB
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Gapop 10.0 , Gapext 0.5
        219241 seqs, 76174552 residues
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63
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Copyright (c) 1993 - 2000 Comp
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      RHSHGG
RHSHG
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I51423
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RHJD13
I50739
I51104
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I51180
I51180
I51180
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RESULT 2 RHSHG gonadolibe C;Species: C;Date: 31 C;Accessio R;Burgus; Proc. Natl A;Title: P	Query Ma Best Loc Matches Qy 1	A;Title: On A;Title: On A;Reference: A;Contents: A;Contents: A;Note: Trp- C;Comment: T C;Superfamil: C;Keywords: F;1/Modified F;10/Modified	A; Molecule A; Residues R; Matsuo,   Biochem. B A; Title: S; A; Reference A; Contents A; Note: the R; Baba, Y.	RESULT 1 RHPGG gonadolibe C,Species: C,Date: 13 C;Accessio R;Baba, Y. BioChem. B A;Title: A;Referenc		44440000000000000000000000000000000000
Oliberin - sheep  scles: Ovis orientalis aries, Ovis ammon aries (dom coles: Ovis Ovis orientalis aries, Ovis orientalis (dom coles: Natl. Acad. Sci. U.S.A. 69, 278-282, 1972  Lle: Primary structure of the ovine hypothalamic luceston, Natl. Acad. Sci. U.S.A. 69, 278-282, 1972	atch 95.2%; Score 60; DB 1; Len cal Similarity 90.0%; Pred. No. 0.00022; 9; Conservative 1; Mismatches 0; EHWSYGLRPG 10 :	.971 LH and FS LH and FS logical acces the secces the secces do (Gln) #status	A; Molecule type: protein A; Molecule type: protein A; Residues: 1-10 (BABA) R; Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V. R; Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V. Riochem. Biophys. Res. Commun. 45, 822-827, 1971 A; Title: Synthesis of the porcine LH- and FSH-releasing A; Reference number: A90176; MUID:72065376 A; Note: the synthetic and natural hormones have the same R; Baba, Y.; Arimura, A.; Schally, A.V.	berin - pig ss: Sus scrofa 13-Jul-1981 #s 100: A01411 Y.; Matsuo, H. Biophys. Res. Structure of snce number: A9	ALIGNMENTS	30 42 66.7 828 2 T08556 31 41 65.1 316 2 A53440 32 41 65.1 532 2 T32849 33 40 63.5 551 2 E64728 34 40 63.5 552 2 B85489 35 40 63.5 565 2 G8243 36 40 63.5 568 2 G8243 37 40 63.5 584 2 J01229 38 39 61.9 345 2 C72710 40 39 61.9 345 2 C72710 41 39 61.9 38 2 C72710 41 39 61.9 501 2 T33827 41 39 61.9 501 2 T32648 42 39 61.9 508 2 T01937 43 39 61.9 1444 2 T18856 44 38 60.3 161 2 D84472 45 38 60.3 293 2 G72699
estic sheep) t_change 18-Mar-1997 , M.; Rivier, J.; Fellows, R.; teinizing hormone-releasing fa	gth 10; Indels 0; Gaps 0;	H-releasing hormone.  ttivity  retion of both luteinizing and  s; pyroglutamic acid  tatus experimental  experimental	hormone by the solid-phase me physicochemical and biologic	change 18-Mar-1997 hormone. II. Confirmation of		hypothetical prote aldose reductase h hypothetical prote yabN protein - Esc probable transport conserved hypothet cellulase (EC 3.2. serine proteinase hypothetical prote

A; Accession: A93780

the same biological activity the secretion of both luteinizing

and

f

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A; Molecule type: protein
A; Residues: 1-10 <BUR>
A; Residues: the natural and synthetic hormones have the same biological activity
A; Note: the natural and synthetic hormones the secretion of both lutein
C; Comment: This hypothalamic hormone stimulates the secretion of both lutein
C; Superfamily: gonadoliberin
C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 10/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: I78541
C;Accession: I78541
R;Ma, Y.J.; Costa, M.E.; Ojeda, S.R.
Reuroendocrinology 60, 346-359, 1994
A;Reiterence number: I58134; MUID:95124501
A;Reference number: I58134; MUID:95124501
A;Accession: I78541
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A;Molecule type: mRNA
A;Residues: 1-67 <RES>
A;Cross-references: GB:S75918; NID:g912831; PIDN:AAI
C;Superfamily: gonadollberin
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N;Alternate names: luteinizing hormone releasing hormone
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pred. No. 0.00022;
1; Mismatches
                                                                      score 60; DB Pred. No. 0.00
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Pred. No. 0.0017;
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A;Cross-references: EMFC;Genetics:
A;Introns: 45/3; 77/3
C;Function:
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gonadoliberin precursor mouse
N;Alternate names: gonadotropin-releasing hormone (GnRH); luteinizing hormone
N;Contains: gonadoliberin; gonadoliberin-associated protein (GAP)
N;Contains: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 18-Mar-1997 #text_change 18-Jun-1999
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A;Accession: A47578
A;Molecule type: DNA
A;Residues: 1-90 <MASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gonadoliberin precursor [validated] - human
NAlternate names: gonadotropin releasing hormone (GnRH); luteinizing hormone releasi
NAlternates names: gonadotropin releasing hormone (GAP); progonadoliberin
NContains: gonadoliberin-associated protein (GAP); progonadoliberin
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 **sequence_revision 21-Jul-1995 **text_change 08-Dec-2000
C;Date: 17-Mar-1987 **sequence_revision 21-Jul-1995 **text_change 08-Dec-2000
C;Accession: 505308; AG6173; A93342; A90108; A01410; S45718
C;Accession: 505308; AG6173; A93342; A90108; A01410; S45718
R;Hayflick, J.S.; Adelman, J.P.; Seeburg, P.H.
Nucleic Acids Res. 17, 6403-6404, 1989
A;Title: The complete nucleotide sequence of the human gonadotropin-releasing hormone
A;Reference number: S05308; MUID:89366682
A;Accession: S05308; MUID:89366682
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A;Molecule type: DNA
A;Residues: 1-92 <HAY>
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Matches 9
                                                                         A; Molecule type: mRNA
A; Residues: 1-92 <ADE>
A; Residues: 1-92 <ADE>
A; Cross references: GB: M12578; NID:g183418;
A; Experimental source: hypothalamus
R; Seeburg, F; H.; Adelman, J.P.
Nature 311, 666-668, 1984
A, Title: Characterization of cDNA for precursor A; Reference number: A93342; MUID:85012739
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; Pred. No. 0.00
1; Mismatches
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C;Function:
A;Description: gonadoliberin stimulates pituitary secretion of lutropin and follitropin A;Description: gonadoliberin associated protein may have prolactin release inhibiting activity C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid F;1-23/Domain: signal sequence **status predicted <SIG>F;24-92/Product: progonadoliberin *status predicted <PGN>F;24-93/Product: gonadoliberin *status experimental <MANT>F;24-33/Product: gonadoliberin *ssociated protein *status predicted <GAP>F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status experim F;34/Modified site: amidated carboxyl end (Gly) (amide in mature form from following c
                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: gonadollberin-associated protein (GAP); gonadotropin N;Contains: gonadollberin; prolactin release-inhibiting factor C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1 C;Accession: A40147; B26173; A48410 R;Bond, C.T.; Hayflick, J.S.; Seeburg, P.H.; Adelman, J.P. Mol. Endocrinol 3, 1257-1262, 1989 A;Title: The rat gonadotropin-releasing hormone: SH locus: structure and A;Reference number: A40147; MUID:89384661 A;Accession: A40147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:GNRH; LHRH; GRH
A;CrOSS-references: GDB:133746;
A;Map postition: 8p21-8p11.2
A;Introns: 47/3; 79/3
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A;Contents: annotation; degradation pathway of synthetic hormone
                                                                                                                                                                                                          R;Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Se Proc. Natl. Acad. Sci. U.S.A. 83, I79-183, 1986 A:Title: Isolation of the gene and hypothalamic A:Reference number: A94090; MUID:86094338 A:Accession: B26173
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A; Title: The chemical identity of the immunoreactive
A; Reference number: A90108; MUID:83126573
A;TItle: Thymocytes express a mRNA that A;Reference number: A48410; MUID:9310548
                                                                  A;Cross-references: GB:M12579; NID:g204445; PIDN:AAA41263.1; R;Maler, C.C.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E. Cell. Mol. Neurobiol. 12, 447-454, 1992
                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-92 <BON>
A;Cross-references: GB:M31670; NID:g204447; PIDN:AAA41264.1;
A;Cross-references: GB:M31670; NID:g204447; Seeburg, P.H.
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A;Molecule type: mRNA
A;Residues: 1-15,'S',17-92 <SEE>
A;Cross-references: GB:X01059; NID:g34356; PIDN:CAA25526.1; PID:g34357
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A; Residues: 1-92 < ADE>
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                                                                                            gonadoliberin I precursor - chicken
N;Alternate names: gonadotropin-releasing hormone I
C;Species: Gallus gallus (chicken)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
C;Accession: I50644; S33507
R;Dunn, I.C.; Chen, Y; Hook, C.; Sharp, P.J.; Sang
J. Mol. Endocrinol. 11, 19-29, 1993
A;Title: Characterization of the chicken preprogona
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A; Accession: I50644
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from

preprogonadotrophin-releasing

hormone-I

Sang,

#text\_change

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A;Introns: 47/3; 79/3
C;Function:
C;Function:
A;Description: stimulates pituitary secretion of lutropin and follitrop A;Description: stimulates pituitary secretion of lutropin and follitrop A;Description: stimulates pituitary secretion may have prolactin release inh C;Superfamily: gonadoliberin
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyr F;1-23/Domain: signal sequence #status predicted <SIG>F;24-92/Product: progonadoliberin #status predicted <PGN>F;24-33/Product: gonadoliberin #status predicted <GLN>F;37-92/Product: grolactin release-inhibiting factor #status predicted F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: amidated carboxyl end (Gly) (amide in mature form fF;33/Modified site: pyrrolidox end (Gly) (amide in mature form fF;33/Modified site: pyrrolidox end (Gly) (amide in mature form fF;33/Modified site: pyrrolidox end (Gly) (amide in mature form fF;33/Modified site: pyrrolidox end (Gly) (Gly) (amide in mature fF;33/Modified site: 
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                                                                                                                                                                                                                                                                                      C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic
F;L/Modified site: pyrrolidone carboxylic acid (Gln) #status experiment
F;10/Modified site: amidated carboxyl end (Gly) #status experimental
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A;Title: Primary structure of two forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: gonadotropin-releasing hormone I
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
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Molecule type: mRNA
Residues: 1-92 <MAI>
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Pred. No. 0.00
2; Mismatches
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Pred. No. 0.0023;
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0.0011;
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RHIDIS
gonadoliberin I precursor - sharptooth catfish
yonadoliberin i precursor - sharptooth catfish
N;Alternate names: gonadoliberin i, gonadoliberin I-associated protein form I; gonadoliberin I-
N;Contains: gonadoliberin I; gonadoliberin I-associated protein form I; gonadoliberin I-
N;Contains: gonadoliberin I; gonadoliberin I-
N;Contains: gonadoliberin I; gonadoliberin I-
C;pactes: Clarias gariepinus (sharptooth catfish)
C;pactes: Clarias gariepinus (sharptooth catfish (clarias gariepinus) (sharptooth catfish)
C;pactes: Clarias gariepinus (sharptooth catfish)
C;pactes: Clarias gariepinu
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A; Residues: 1-92 <DDZ>
A; Cross references: EMBL:X69491;
C; Genetics:
A; Introns: 47/3; 79/3
C; Superfamily: gonadoliberin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; White, S.A.; Kasten, T.L.; Bond, C.T.; Adelman, J.P.; Fernald, R.D.

Proc. Natl. Acad. Sci. U.S.A. 92, 8363-8367, 1995
A; Title: Three gonadotropin-releasing hormone genes in one organism suggest novel roles A; Reference number: I50739; MUID:95396797
A; Recession: I50739; MUID:95396797
A; Rocession: Procession: Title RNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-98 < MHID
A; Residues: 1-98 < MHID
A; Residues: 1-98 < MHID
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C;Species: Haplochromis burtoni
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 150739
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C;Superfamily: gonadoliberin
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8; Conserv
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80.0%;
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A; Experimental source: brain C; Superfamily: gonadoliberin C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid C; Keywords: asignal sequence #status predicted <SIG> F; 1-21/Domain: signal sequence #status predicted <MATI> F; 22-31/Product: gonadoliberin I #status experimental <MATI> F; 35-80/Product: gonadoliberin I-associated protein #status predicted <MAT2> F; 32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form from ff; 31/Modified site: amidated carboxyl end (Gly) (amide in mature form from ff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medaka-type gonadotropin-releasing hormone precursor - Japanese medaka C;Species: Oryzias latipes (Japanese medaka) C;Decies: Oryzias latipes (Japanese medaka) C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000 C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000 C;Date: Novel form of yoshiura, Y.; Suetake, H.; Aida, K. R;Okubo, K.; Amano, M.; Yoshiura, Y.; Suetake, H.; Aida, K. R;Okubo, K.; Amano, M.; Yoshiura, Y.; Suetake, H.; Aida, K. R;Okubo, K.; Amano, M.; Yoshiura, Y.; Suetake, H.; Aida, K. R; Aida,
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A; Residues: 1-91 <OKU>
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A; Contents: JC7393
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A;Cross-references: DDBJ:AB041333
C:Comment: This protein plays the
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C;Species: Oncorhynchus keta (chum salmon)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A21114
R;Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivler, J.; Vale, W. R;Sherwood, N.; Eiden, L.; Brownstein, 1983
Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983
A;Title: Characterization of a teleost gonadotropin-releasing hormone. A;Feference number: A21114; MUID:83195140
A;Accession: A21114
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A; Status: preliminary
A; Molecule type: protein
A; Molecule type: protein
A: Passidues: 1-10 <SHE>
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A; Residues: 1-10
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   QHWSYGWLPG
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7; Conserv
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Pred. No.
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                                                                                                                                              Score 47; DB 2; pred. No. 0.036; 1; Mismatches
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gonadotropin-releasing hormone - cherry salmon C;Species: Oncorhynchus masou (cherry salmon) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Aug-1997 C;Accession: I51180 R;Suzuki, M.; Hyodo, S.; Kobayashi, M.; Aida, K.; Urano, A. J. Mol. Endocrinol. 9, 73-82, 1992 A;Title: Characterization and localization of mRNA encoding the salmon-type gonadotrophi A;Reference number: I51180; MUID:92384893 A;Accession: I5180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gonadotropin releasing hormone - chinook salmon (fragment)
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Aug-1997
C;Accession: I51092
R;Klungland, H.; Lorens, J.B.; Andersen, O.; Kisen, G.O.; Alestrom, P.
Moi. Cell. Endocrinol. 84, 167-174, 1992
A;Title: The Atlantic salmon prepro-gonadotropin releasing hormone gene and mRNA.
A;Reference number: I51040; MUID:92267241
A;Accession: I51092
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A;Residues: 1-74 <KLU>
A;Cross-references: EMBL:X79711; NID:g499322; PID:g499323
Search completed: November 13, 2001, 14:28:18 Job time: 124 sec
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A;Molecule type: mRNA
A;Residues: 1-82 <SUZ>
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A; Introns: 38/3; 65/3
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24 QHWSYGWLPG 33
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517; AAA034 80; RHSHG. IPRO2012; 0446; GnRH; PS00473; GN on pair of 1 1 1 1 1 3	ROT ent Swiss Bioinf -profit this s uires a	1-10. 4314; P utcher Blackwe Blackwe ucture ctor (L ctor (A ctor (B ct	NRH OR LHRI (Sheep); (Sheep); Metazoa; Eutheria; (Eutheria; O'aprinae; O'aprinae; F 12-61 FRO FTERN RANGE: FR.E., Wise (OCT-1993)	STAND (Rel. 37 (Rel. 37 (Rel. 39 ERIN I P HORMONE GNRH I)	601.9
03433.1; 1G; 1G; 1G; 1C; 1C; 1C; 1C; 1C; 1C; 1C; 1C; 1C; 1C	BELONGS TO entry is constitution informatic institution fit institution is a licens.	PubMed=45 M., Amos ell R., v of the of the-eptide-Ed Sci. U.S. ULATES TH OF BOTH L	Getartic Covis. PROM N.A. 3E; TISSUI 3E M.E.; 3) to the	ARD; , Crea , Last , Last RECURS RELEA (LULIB	86 1 86 1 110 1 110 1 120 1 120 1 110 1 551 1 584 1 10 1 432 1
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nidation; Hypothalamus; c. PPTIDE I.	ed through a collaboration and the EMBL outstation re no restrictions on its something by and for commercial //www.isb-sib.ch/announce/	n M., Rivier J., einizing hormone- chromatography-mass chropins; it stimulates	Pecora; Bovoidea;	BERIN I (LHRH I) OTROPIN RELEASING ED PEPTIDE I)	P43306 clarias gar 042241 oncorhynchu 042241 oncorhynchu 091330 rutilus rut 097686 suncus muri 095336 tupaia glis 043555 homo sapien P96769 actinobacil P45377 mus musculu P33595 escherichia P25472 clostridium P30948 petromyzon P55495 rhizobium s

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30-MAY-2000 (Rel. 39, Last annotation update)
PROGONADOLIBERIN I PRECURSOR (CONTAINS: GONADOLIBERIN I (LH
PROGONADOLIBERIN I PRECURSOR HORMONE I) (GONADOTROPIN REL
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN REL
HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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AMIDATION (G-11 PROVIDE AMIDE GROUP).
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AMIDATION (
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING LUTEINIZING HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I]
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuroendocrinology 60:346-359(1994).

-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STIMULATES
THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Hypothalamus;

MEDLINE-95124501; PubMed-7545971;

MA Y J. (Osta M.E., Ojeda S.R.;

"Developmental expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor alpha and its receptor in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE GNRH FAMILY.
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EHWSYGLRPG 10
                                                                                                                                                                                                                                                                                                                                                                            PF00446;
                                                                                                                                                                                                                                                                                                                                                                                                            S75918; AAB33096.1;
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                                 Similarity
9; Conser
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                                                                                                                                                                                                                                                                                                                                           pair
                                 Conservative
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7573
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ACTIVITY (BY SIMILARITY).
ACTIVITY (BY SIMILARITY).
PYROLIDONE CARBOXYLIC AC
SIMILARITY).
AMIDATION (G-16 PROVIDE A
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                  score 60; DB 1;
Pred. No. 0.00042;
1; Mismatches
                                                                                                                                                                                                                                                 GNRH-ASSOCIATED PEPTIDE
                                                                                                                                                                                                                                                                 GONADOLIBERIN I.
                                                                                                                      505394DAA261A3F2
                                                                                                                                                                                                                                                                                  PROGONADOLIBERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                    Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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i; Cercopithecidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AΑ
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                                                                                                                                                                                                                                                                                                                                                      Amidation; Hypothalamus;
                                                                       Length 67;
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                                             Indels
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                                                                                                                                                                           AMIDE GROUP) (BY
                                                                                                                                                                                                                                          BIOLOGICAL
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QHWSYGLRPG

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                             01-JAN-1990 (Rel. 13
01-JAN-1990 (Rel. 13
30-MAY-2000 (Rel. 39
PROGONADOLIBERIN I F
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                                                                                                                     GON1_MOUSE
P13562;
01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE
MOD_RES
MOD_RES
SEQUENCE
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PEPTIDE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94165563; PubMed-8137750;
Hayes W.P., Wray S., Battey J.F.;
"The frog gonadotropin-releasing hormone-I (GnRH-I) gene has
mammalian-like expression pattern and conserved domains in
GnRH-associated peptide, but brain onset is delayed until
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GON1_XENLA STANDARD; PRT; 89 AA. P45656; P01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) GONADOLIBERIN I PRECURSOR (GONADOTROPIN-RELEASING GONADOLIBERIN I PRECURSOR (GONADOTROPIN-RELEASING GONADOTROPIN-RELEASING GONADOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GnRH-associated peptide,
metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LH-RH) (LULIBERIN I).
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage on
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(LUTEINIZING
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9; Conserv
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0446; GnRH; 1.
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HORMONE
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                                                                                                                                                                                      STANDARD;
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                13, Created)
13, Last sequence update)
39, Last annotation update)
1 PRECURSOR (CONTAINS: GONADOLIBERIN I
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RELEASING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 1;
Pred. No. 0.00056;
1; Mismatches (
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AMIDATION (G-34 PROVIDE AMIDE GROUP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6F4F36FBAE0D4284
HORMONE I) (GONADOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hormone; Amidation; Hypothalamus;
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                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HORMONE ASSOCIATED
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(LHRH I)
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RESULT
GON1_PIG
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MOD_RES
SEQUENCE
                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOTROPIN RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I].
                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phillips H.S., Nikolics K., Seeburg P.H.;
"A deletion truncating the gonadotropin-releasing responsible for hypogonadism in the hpg mouse.";
Science 234:1366-1371(1986).
-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTE THE SECRETION OF BOTH LUTBINIZING AND FOLLICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M14872; AF MGD; MGI:95789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                         Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                     P49921;
                                                                                                                                                                                 GON1_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage
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           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mason A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87069928; PubMed=3024317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HORMONE I) (GNRH I) (LULIBERIN I); PROLACTIN RELEASE-INHIBITING FACTOR
TISSUE=Hypothalamus
                                 NCBI_TaxID=9823;
                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                            22 QHWSYGLRPG
                                                                                                                                                                                                                                                                   1 EHWSYGLRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M14872; AAA37717.1;
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                                                                                                                                                                                                                                                                                          Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              on pair of basic; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00473;
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Metazoa; Chordata; C
Metazoa; Rodentia; S
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                                                                                                                                                                                                                                                                                           Conservative
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31
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                                               Cetartiodactyla;
                                                          Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                     95.2%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues;
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PROLACTIN RELE
APPEARS TO BE
                                                                                                                                                                                                                                                                                                     Pred. No. 0
                                                                                                                                                                                                                                                                                                                  Score 60;
                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-32 P)
1C0766FA4826E4D9
                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNRH
                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; Amidation; Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY
                                                Suina; Suidae;
                                                                                                                                                                                 91
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D BE ESSENTIAL FOR I
                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muridae;
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D9 CRC64;
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                                                Sus
                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                  AMIDE GROUP)
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MBL outstation -
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baba Y., Matsuo H., Schally A.V.;
"Structure of the porcine LH- and FSH-r
Confirmation of the proposed structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=72065376; PubMed=4942726; Matsuo H., Arimura A., Nair R.M.G "Synthesis of the porcine LH- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 44:459-463(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=72114303; PubMed=4946067;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phase method.";
GON1_HUMAN STANDARD;
GON1_HUMAN STANDARD;
P01148;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1988 (Rel. 07, Last sequence update)
01-APR-1988 (Rel. 07, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
PROGONADOLIBERIN I PRECURSOR (CONTAINS); GONADOTROPIN RELEASING
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADORELIN); GNRH-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNTHESIS OF GONADOLIBERIN.
MEDLINE=72117544; PubMed=4946275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
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                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the tryptophan residue in porcine LH and FSH-releasing horr chem. Biophys. Res. Commun. 45:483-487(1971). FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STITHE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE GNRH FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A01411;
                                                                                                                                                                                                                                                                                                                    EHWSYGLRPG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L32864; AAA31066.1;
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                                                                                                                                                                                                                                                                                                                                                                similarity
9; Conserv
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GONADOLIBERIN I.
GONH-ASSOCIATED PEPTIDE I.
APPEARS TO BE ESSENTIAL FOR BIT
ACTIVITY.
ACTIVITY.
PYRROLIDONE CARBOXYLIC ACID.
PYRROLIDON (G-34 PROVIDE AMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Becker B.A.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .M.G., Schally A.V.; and FSH-releasing hormone
                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 1;
pred. No. 0.00057;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45:822-827(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone; Amidation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothalamus;
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Adelman J.P., Mason A.J., Hayflick J.S., Seebur "Isolation of the gene and hypothalamic cDNA fo of gonadotropin-releasing hormone and prolactin factor in human and rat.";

Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE=86094338; PubMed=2867548; MEDILINE=86094338; PubMed=2867548; Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.; Adelman J.P., Mason A.J., Hayflick J.S., Mason A.J., Hayflick J.S., Seeburg P.H.; Adelman J.P., Mason A.J., Hayflick J.S., Mason A.J., Hayflick J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=89366682; PubMed=2671939;
Hayflick J.S., Adelman J.P., Seeburg
"The complete nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biosynthesized in the human placenta.";
Biochem. Biophys. Res. Commun. 109:1061-1071(1982).
-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT ST.
THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of cDNA releasing hormone.";
Nature 311:666-668(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85012739; PubMed=6090951; MEDLINE=85012739; Adelman J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic
                  MOD_RES
MOD_RES
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
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                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                MIM;
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PEPTIDE
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                                                                                                                                                                                                  Placenta;
                                                                                                                                                                                                                                                                             InterPro;
    SEQUENCE
                                                                                                                                                                               SIGNAL
                                                                                                  ACT_SITE
                                                                                                                                                                                                                                                                                                             BL; X01059; CAA25526.1; -
BL; M12578; AAA35916.1; -
R1; X15215; CAA33285.1; -
R1; A01410; RHUG.
R; A26173; A26173.
R; S05308; S05308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHARMACEUTICAL: AVAILABLE UNDER LUTREPULSE OR LUTRELEF (FERRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L., Rousseau P., chemical identity of the immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUTREPULSE OR LUTRELEF
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                                                                                                                                                                                                                       on.
                                                                                                                                                                                                                                          PS00473;
                                                                                                                                                                                                    Pharmaceutical;
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      92
                                                                                                                                                                                                                     00473; GNRH; 1. pair of basic
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Primates;
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          MW.
                                                                                                                                                                                                        Signal.
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                                                                                                      GONADOLIBERIN I.
GNRH-ASSOCIATED F
APPEARS TO BE ESS
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        AMIDATION (G-34 P)
W -> S (IN REF. 3)
30A72221B076FA79
                                                                  ACTIVITY.
PYRROLIDONE CARBOXYLIC
                                                                                                                                                                   PROGONADOLIBERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE NAMES FACTREL (AYERST LABS), PHARMACEUTICALS) AND RELISORM
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                                                                                                            ESSENTIAL
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                                                        AMIDE GROUP).
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                                                                                                                  BIOLOGICAL
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GON1_RAT
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                                                                                                                                                                                           DNA locu
Science
-I- FUNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86094338; PubMed-2867548; Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.; *Isolation of the gene and hypothalamic cDNA for the cof gonadotropin-releasing hormone and prolactin releas factor in human and rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GON1_RAT P07490;
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               Maior C.C., Marchetti B., Leboeuf R.D., Blalock J.E.; "Thymocytes express a mRNA that is identical to hypothalamic lutelnizing hormone-releasing hormone mRNA."; Cell. Mol. Neurobiol. 12:447-454(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-89384661; PubMed-2476669;
Bond C.T., Hayflick J.S., Seeburg P.H., ,
"The rat gonadotropin releasing hormone:
                                                                                                                                                                                                                                              MEDLINE-87149087; PubMed-3547652; Adelman J.P., Bond C.T., Douglass
                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Thymus;
MEDLINE-93105480; PubMed-1468115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
Mammalia;
                                                                                                                                   -!- SIMILARITY:
                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-47 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothalamic expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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                                                                                                                                  TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                           FUNCTION:
                                                                                                                                                                                                                     locus."
                                                                                                                                                                HORMONES
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                                                                                                                                                                                                                                mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          norvegicus (Rat)
                                                                                                                                                                     235:1514-1517(1987).
CTION: STIMULATES THE SECRETION OF GONADOTROPINS: IT STIMULATES SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conser
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    (LULIBERIN I);

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Rodentia;
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Pred.
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                              Herbert E.;
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locus: structure
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Murinae; Rattus.
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I].
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EMBL; M31670; AAA41264.1; -.
EMBL; M15527; AAA42141.1; ALT_SEQ.
EMBL; M15529; AAA42139.1; -.
EMBL; M15528; -; NOT_ANNOTATED_CDS.
PIR; B26173; RHRTG.
                                                                                                                                                                                                                                               TISSUE-Hypothalamus;
MEDLINE-97079639; PubMed-8921350;
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                     GON1_TUPGB
Q95335;
                                          use by non-profit institutions as long as modified and this statement is not removed. Usentities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                      between the Swiss Institute of Bioinfo
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                          GNRH1 OR GNRH
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                     EMBL; U63326; AAB16837.1;
                                                                                                              This
                                                                                                                                                                                          placental mammal."
                                                                                                                                                                                                                           Fernald R.D.;
                                                                                                                                                                                                                                       Kasten
                                                                                                                                                                                                                                                                                                                            Tupaia glis belangeri (Common tree shrew)
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           InterPro
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                                                                                                                                     SIMILARITY:
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                                                                                                 SWISS-PROT entry is copyright. It is produced through a seen the Swiss Institute of Bioinformatics and the EMBL
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Similarity 90.0%;
9; Conservative
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                                                                                                                                                                               Endocrinol. 104:7-19(1996)
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                                                                                                                                    BELONGS TO THE GNRH FAMILY.
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Scandentia; Tupaiidae; Tupaia.
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33
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mesencephalic GnRH c
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1; Mismatches
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PYRROLIDONE CARBOXYLIC ACID.

AMIDATION (G-34 PROVIDE AMIDE GROUP)
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GONADOLIBERIN I.
PROLACTIN RELEASE-INHIBI
APPEARS TO BE ESSENTIAL
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                                                      (See http://www.isb-sib.ch/announce/
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D BE ESSENTIAL FOR E
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p37041; p20407;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
GONADOLLEBRIN I (GONADOTROPIN-RELEASING HORMO
(LULIBERIN I).
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I_CHICK S
GON1_CHICK S
P37042; P20407;
01-FEB-1991 (Rel
                                                                                                                                                                                                                                                     MEDLINE=91352338; PubMed=1882082;
Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
"Primary structure of two forms of gonadotropin-releasing hormone
from brains of the American alligator (Alligator mississippiensis).";
                                                                                                                                                                                                                                                                                                                                         Alligator mississippiensis (American alligator).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Crocodylidae; Alligatorinae; Alligator
                                                                                                                                                             Hormone;
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                               SEQUENCE.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8496;
                                                                                                                                                                                                           PIR; A60066; RHAQ1.
InterPro; IPR002012;
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                                                                 EHWSYGLRPG
                                                                                                                                                                                          PF00446; GnRH; 1.
rE; PS00473; GNRH; 1
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9; Conser
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on pair of bas
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8; Conser
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                     STANDARD;
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90.0%;
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                                                                                                                                                                                                                                         THE SECRETION OF GONADOTROPINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score 60; DB Pred. No. 0.00
                                                                                                        ; Score 56; DB
; Pred. No. 0.00
2; Mismatches
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GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE
APPEARS TO BE ESSENTIAL
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PYRROLIDONE CARBOXYLIC
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                PYRROLIDONE CARBOXYLIC AMIDATION.
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                         PRT;
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    I) (GNRH-I) (LH-RH

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30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last sequence update)
40-MAY-2000 
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STRAIN-WHITE LEGHORN;
STRAIN-H9405935; PubMed=7902095;
Dunn I.C., Chen Y., Hook C., Sharp P.J., Sang H.M.;
"Characterization of the chicken preprogonadotrophin-releasing "Characterization of the chicken preprogonadotrophin-releasing bormone-I gene;";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Hypothalamus;
MEDLINE-82265778; PubMed=7050119;
King J.A., Millar R.P.;
Structure of chicken hypothalamic luteinizing hormone. II. Isolation and characterization.";
J. Biol. Chem. 257:10729-10732(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDITME-82265777; PubMed=/0304440, MEDITME-82265777; PubMed=/0304440, King J.A., Millar R.P.; King J.A., Millar R.P.; "Structure of chicken hypothalamic luteinizing hormone-releasing "Structure of chicken hypothalamic non partially purified ......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Mol. Endocrinol. 11:19-29(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Hypothalamus;
King J.A., Millar R.P.;
"Structure of avian hypothalamic
S. Afr. J. Sci. 78:124-125(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 24-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 257:10722-10728(1982).
-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
-i- SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                       PEPTIDE
PEPTIDE
MOD_RES
MOD_RES
SEQUENCE
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SIGNAL
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$33507; $33507.
       EHWSYGLRPG
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8; Conser
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GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE I.
PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-34 PROVIDE AMIDE G
1; 61AEB7EBAF508B6A CRC64;
                                                      Score 56; DB pred. No. 0.00 2; Mismatches
                                                        2;
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                                                                                                        DΒ
                                                                                  .0029;
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                                                                                                        Length 92;
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**QHWSYGLQPG** 

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JLT 12
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GON1_HAPBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GONADCLIBERIN I PRECUSOR (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)
(LH-RH I) (LULIBERIN I).
PEPTIDE PEPTIDE MOD_RES
                                                    Signal;
SIGNAL
                                                                                                                                                                       the European Bioinformatics Institute. The by non-profit institutions as low modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   and pumpkinseed fish.";
Regul. Pept. 57:43-53(1995)
-:- FUNCTION: STIMULATES TH
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P51918; 093387;
01-OCT-1996 (Re
                                       CHAIN
                                                                                                                   EMBL; U31865; AAC59691.1; -. EMBL; AF076961; AAC27716.1; InterPro; IPR002012; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White S.A., Kasten T.L., Bond C.T., Adelman J.P., "Three gonadotropin-releasing hormone genes in on novel roles for an ancient peptide.";
Proc. Natl. Acad. Sci. U.S.A. 92:8363-8367(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Pituitary;
MEDLINE-95372591; PubMed-7644702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Ontogeny of gonadotropin-releasing hormone (GnRH) gene expression reveals a distinct origin for GnRH-containing neurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-99061842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherwood N.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Powell J.F.F., Fischer W.H., Park White S.A., Francis R.C., Fernald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White R.B., Fernald R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-8153;
                                                                              Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                         Primary structure of solitary form of gonadotropin-releasing hormone (GnRH) in cichlid pituitary; three forms of GnRH in brain of cichlid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF
                                                                                                                                                                                                                                                                                               GONADAL AXIS.
TISSUE SPECIFICITY: SYNTHESIZED IN PREOPTIC NEURONS AND I TRANSPORTED TO THE PITUTARY IN THE PREOPTIC-HYPOPHYSEAL MASS SPECTROMETRY: MW-1113.9; METHOD-MALDI; RANGE-23-32.
                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                                                                                                                                                                                     FUNCTION: STIMULATES THE SECRETION OF RESPONSIBLE FOR THE REGULATION OF THE
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                                                                                                         PF00446; GnRH; 1
                                                                  Multigene
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on pair of basic
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                                                                  family.
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                                                                              residues; Hormone;
GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE
PYRROLIDONE CARBOXYLIC A
                                       PROGONADOLIBERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               M., Craig A.G., R.D., Licht P.,
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                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in one
                                                                              Amidation; Hypothalamus;
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Warby C
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organism suggest
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              (POTENTIAL)
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P70074;
15-JUL-1998
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CONFLICT
SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Sparidae; Chrysophrys.
NCBI_TaxID-8171;
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15-DEC-1998 (Rel. 37, Last annotation update)
GONADOLIBERIN I PRECURSOR (GONADOTROPIN-RELEASING
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SIGNAL 1
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                                                                                                                                                                           SEQUENCE
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                      1 EHWSYGLRPG : | | | | | | |
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QHWSYGLSPG
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                                                                                                                                                                                                                                                                                                                                                                             residues; Hormone;
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Pred.
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61E79C990328D73E CRC64;
                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC SIMILARITY).
                                                                                                                                                                                                                                                                              GUNADULIBERIN I.
GNRH-ASSOCIATED PEPTIDE
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E57DBA83333278D7
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ENGHRTFKK -> KMDTGHSRNERFL (IN REF.
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No.
                                                                                                 54; DB 1;
No. 0.0067;
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278D7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
GONADOLIBERIN I PRECURSOR (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)
(LH-RH I) (LULIBERIN I) (SBGNRH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Powell J.F.F., Zohar Y., Elizur A., Park M., Fischer W.H., Craig A.G., Rivier J.E., Lovejoy D.A., Sherwood N.M.; Three forms of gonadotropin-releasing hormone characterized brains of one species."; D.S.A. 91:12081-12085(1994).

Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).

-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.

-i- MASS SPECTROMETRY: MW-1113.6; METHOD-MALDI; RANGE-26-35.

-i- SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95268499; PubMed-7749463; Gothilf Y., Elizur A., Chow M., Chen T.T., Zohar Y.; Gothilf Y., Elizur A., Chow M., Chen T.T., Zohar Y.; Molecular cloning and characterization of a novel gonadotropin-releasing hormone from the gilthead seabream (Sparus aurata)."; Mol. Mar. Biol. Biotechnol. 4:27-35(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P51919;
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sparidae; Sparus.
NCBI_TaxID=8175;
 GON1_CAVPO
O54713;
15-DEC-1998 (
15-DEC-1998)
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                                                         CAVPO
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                                                                                                                26 QHWSYGLSPG
                                                                                                                                            1 EHWSYGLRPG
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Pred. No.
1; Mismatcl
       sequence
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GONADOLIBERIN I.
GONAPOLIBERIN I.
GONRH-ASSOCIATED PEPTIDE I (POTENTIAL)
PYRROLIDOME CARBOXYLIC ACID.
AMIDATION (G-36 PROVIDE AMIDE GROUP)
49313FD6FD6B87DA CRC64;
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Search completed: November 13, Job time: 395 sec

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                                                                            Query Match
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PROGONADOLIBERIN I PRECURSOR [CONTAINS: GONADOLIBERIN I (LHRH I)
(LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING
HORMONE I) (GNRH I) (LULIBERIN I); GNRH-ASSOCIATED PEPTIDE I].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-HARTLEY WHITE; TISSUE-Hypothalamus;
MEDLINE-97462693; PubMed=9322920;
bihin R S., King J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNRH1 OR GNRH OR LHRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrinology 138:4123-4130(1997).
-i- FUNCTION: STIMULATES THE SECRETION
THE SECRETION OF BOTH LUTEINIZING A
                                                                                                                                                                                                                                                          Placenta;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reveals a unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jimenez-Linan M., Rubin B.S., King J.C.;
"Examination of guinea pig luteinizing hormone-releasing hormone in account of guinea pig luteinizing hormone-releasing hormone in the same of two transcripts in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10141;
                                                                                                                                                                                                                PEPTIDE
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                                                                                                                       SEQUENCE
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 24
                         1 EHWSYGLRPG
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QYWSYGVRPG
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                                                                   81.0%;
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                                                                                                                                                                           GONADOLIBERIN I.
GONRH-ASSOCIATED PEPTIDE I.
APPEARS TO BE ESSENTIAL FOR
ACTIVITY (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleosto
Hystricognathi; Caviidae; Cavia
                                                      Score 51; DB 1;
Pred. No. 0.022;
3; Mismatches
                                                                                                                                       SIMILARITY)
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AND
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                                                                                                                                                     G-34 PROVIDE AMIDE
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                                                                                    Length 92;
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5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_unclassific
13: sp_vertebrate:
14: sp_virus:*
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1 EHWSYGLRPG 10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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94	94	90	90	88	82	82	82	82	33	33	10	10	91	90	99	95	87	91	Query Match Length
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Q9DEH5	Q9DEH6	Q9DD49	Q9IA09	Q9PSY9	Q918P9	091800	Q9W7G1	Q92094	Q9PT34	Q9W7G0	P81751	P81749	Q9DGC8	Q9IAU2	Q9IA10	073812	Q9YI26	Q9PRH0	ID
Q9deh5 carassius a	Q9deh6 carassius a	Q9dd49 oryzias lat	Q9ia09 dicentrarch	Q9psy9 sparus aura	Q9i8p9 oncorhynchu		Q9w7g1 oncorhynchu	Q92094 oncorhynchu	Q9pt34 oncorhynchu	Q9w7g0 oncorhynchu	P81751 clupea pall	_	Q9dgc8 oryzias lat	Q9iau2 rana dybows	Q9ia10 dicentrarch	073812 morone saxa	Q9yi26 sparus aura	Q9prh0 anguilla ja	Description

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61.9	61.9	61.9	61.9				63.5		65.1	65.1	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	74.6
417	388	379	322	101	1000	565	283	532	316	315	828	686	114	107	93	87	86	86	86	85	85	80	75	10	94
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Q9TXI2	Q9YD14	Q9LV12	Q9F3C9	079746	Q9PCD0	Q9KM11	Q9F2U4	044866	008782	P91045	Q9SZR5	Q9H6R3	097655	Q9TSI3	Q9DG36	Q9PRI3	Q9PT25	Q9PW69	042471	Q91A08	073811	Q9DGC9	Q9TTV0	P81750	Q9DDD8
Q9txi2 caenorhabdi	Q9yd14 aeropyrum p	Q91v12 arabidopsis	Q9f3c9 streptomyce	079746 omanosaura	Q9pcd0 xylella fas	Q9km11 vibrio chol		O44866 caenorhabdi	008782 cricetulus	P91045 caenorhabdi	Q9szr5 arabidopsis	Q9h6r3 homo sapien	097655 macaca mula	Q9tsi3 macaca mula	Q9dg36 rana catesb	Q9pri3 anguilla ja	Q9pt25 oncorhynchu	Q9pw69 typhlonecte	O42471 carassius a	-	073811 morone saxa	Q9dgc9 oryzias lat	Q9ttv0 trichosurus	P81750 clupea pall	Q9ddd8 brachydanio

## ALIGNMENTS

S T T T W R R R R R R R R R R R R R R R R	RESULT
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Best Local S
Matches 8
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Q9YI26;
Q9YI26;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TremBLrel. 10, Created)
01-MAY-1999 (TremBLrel. 10, Last sequence update)
01-MAR-2001 (TremBLrel. 16, Last annotation update)
G0NADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
(LULIBERIN) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sparus aurata (Gilthead sea bream).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostel;
Acanthomorpha; Acanthopterygii; Percomor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sparidae; Sparus.
NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nabissi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -73812 PRELIMINARY; PRT; 95 AA.

073812;
073812;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MG-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
001-MAR-1001 (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Kight K.E., Gothilf Y., Alok D., Zohar Y.; Chow M.M., Kight K.E., Gothilf Y., Alok D., Zohar Y.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databass submitted (MAR-1998) to the EMBL/GenBank/DDBJ databass.-

-!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPI.

-!- SIMILARITY: TO THE GNRH FAMILY.

EMBL; AF056314; AAD03817.1; -.
                                                                                                                                                                                                                                                                    Moronie sazitilis (Striped bass).
Morone Sazitilis (Striped bass).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Acanthomorpha; Acanthopterygii; Percomor
Moronidae; Morone.
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                                                                                                                                                                                                                                       NCBI_TaxID=34816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LULIBERIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            بــــ
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EUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
SIMILARITY: TO THE GNHH FAMILY.
L; AF046801; AAD02427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||||||||||
QHWSYGLRPG
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:|||||| ||
1 QHWSYGLSPG
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9; Conserv
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8; Conser
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87
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87
9871 MW;
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90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pred. No. 0.03
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0D2463533D96782A CRC64;
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:leostei; Euteleostei; Neoteleostei;
Percomorpha; Perciformes; Percoide
                                                                                                                                                                                                                                                                                                                          Percomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
0.031;
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                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostom1;
Euteleoste1; Neoteleoste1;
rpha; Perciformes; Percoide1;
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                                                                                          ODBJ databases
GONADOTROPINS
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01-OCT-2000 (
01-OCT-2000 (
01-MAR-2001 )
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
60NADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gonzalez-Martinez D., Madigou T., Zmora N., Anglade I., Zohar Y., Elizur A., Munoz-Cueto J.A., Kah O.; Zohar Y., Zoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dicentrarchus labrax (European sea bass).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Actinopterygii; Neopterygii; Percomorpha; Perciformes; Percoide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moronidae; Dicentrarchus
Q9IAU2;
Q9IAU2;
01-OCT-2000
01-OCT-2000
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00473; GNRH; 1.
Amidation; Hormone.
SEQUENCE 99 AA; 10758 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPROUZULZ;
Pfam; PF00446; GnRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: STIMULATES
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                                                                                                                                                                                                                                                                                                                               1 EHWSYGLRPG
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                                                                                                                                                                                                                                                                         QHWSYGLSPG
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                            85.7
nilarity 80.0
Conservative
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   (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 16,
                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
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                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dicentrarchus labrax.";
EMBL/GenBank/DDBJ databases
E SECRETION OF GONADOTROPINS
            Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 13
Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EC8AEEC93CC02904 CRC64;
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  perciformes; Percoidei;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 99;
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Best Local S
Matches 8
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                                                                                                Biochem. Biophys. EMBL; ABO41333; BAICHAIN 22
SEQUENCE 91 AA;
                                                                                                                                                                                      MDGNRH.

Oryzias latipes (Medaka fish).

Oryzias, Metazoa; Chordata; Craniata; Vertebrata; Euteleos Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteles Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.

NCBI_TaxID=8090;
                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PREPRO-GONADOTROPIN-RELEASING HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a Novel Gonadotropin-Releasing Mol. Cell. Endocrinol. 0:0-0(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                         PubMed-11006121;
                                                                                                                                                                 TISSUE-BRAIN;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              Q9DGC8;
                                                                                                                                                                                                                                                                                        Q9DGC8
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000303; -; 1. PROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001211;
InterPro; IPR002012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF139911; AAF44343.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kwon H.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YOO M.S., Kang H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana dybowskii (Frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LULIBERIN)
                                                                                                                                atipes."
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                         22
                                        1 EHWSYGLRPG 10
                                                                        Match
                                                                                                                                        Novel Form of
                                                                                                                                                                                                                                                                                                                                               1 EHWSYGLRPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION:
                                                                                                                                                                                                                                                                                                                               QHWSFGLSPG 31
                                                                                                                                                                                                                                                                                                                                                               Similarity 80.8; Conservative
                                                        Similarity
7; Conserv
                                                                                                                                                Amano M., Yoshiura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endocrinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                                                                                Hormone.
                                                         Conservative
                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              docrinol. 0:0-0(2000)
STIMULATES THE SECRE
                                                                                                               s. Res. Comm
BAB16303.1;
                                                                                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO THE GNRH
                                                                                                                                       M., Yoshiura Y., Suetake
Gonadotropin-Releasing F
                                                                                                                                                                                                                                                                                                                                                                                                        10368 MW;
                                                                                                 10307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Distribution and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                       82.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anura;
                                                                79
                                                                                                                       Commun.
                                                                .0%;
                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a; Craniata; V
Neobatrachia;
                                                                                                                                                                                                                                                                                                                                                               Score 52; DB
Pred. No. 0.07
1; Mismatches
                                                        Score 50; DB 13
Pred. No. 0.16;
2; Mismatches
                                                         <u>ب</u>
                                                                                                GONADOTROPIN-RELEASING HORMONE A00F2BED6FD6E0B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECRETION
                                                                                                                                                                                                                                                                                                                                                                                                        C3D573E78B52ABFA CRC64;
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                        276:298-303(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phamacological
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                                                                                                                                                                                                                                                                                                                                                                       DB 13
0.071;
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a; Ranoidea;
                                                                                                                                       Hormone
                                                                                                                                                Ξ.
                                                                                                                                                                                                                                                                                        Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GONADOTROPINS
                                                                       13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Troskie
                                                                                                                                                                                                                                                       update)
                                                                                                                                                 Aida K.;
                                                                                                                                                                                                                                                                                                                                                                              Length 90
                                                                       Length 91
                                                                                                                                        in
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                                                         Indels
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                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Characterization
                                                                                                                                                                                                               Euteleostomi;
Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LH-RH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Millar
                                                                                                                                        Medaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frog
                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brain.";
                                                                                                                                        Oryzias
                                                         Gaps
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Best Local
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MOD_RES
MOD_RES
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 SEQUENCE
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SEQUENCE, AND FUNCTION.

SEQUENCE, AND FUNCTION.

TISSUE-BRAIN, AND PITUITARY;

MEDLINE=20114351; PubMed=10650929;

Carolsfeld J., Powell J.F., Park M., Fischer W.H., Craig A.G.,

Chang J.P., Rivier J.E., Sherwood N.M.;

Primary structure and function of three gonadotropin-releasing

hormones, including a novel form, from an ancient teleost, herri

Endocrinology 141:505-512(2000).

-!- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND

FOLLICLE-STIMULATING HORMONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN, AND PITUITARY:
MEDLINE-2011/4351; PubMed-10650929;
Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.
Chang J.P., Rivier J.E., Sherwood N.M.;
"Primary structure and function of three gonadotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P81749 PRELIMINARY; PRT; 10 AA.
P81749;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GONADOLLBERIN I (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P81751 PRELIMINARY; PRT; 10 AA.
P81751;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HORMONE III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LH-RH) (LULIBERIN I).
Clupea pallasii (Pacific herring).
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Clupeinae; Clupea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinopterygii; Neopterygii; Teleostei; Clupeinae; Clupea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clupea pallasii (Pacific herring).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hormones, including a novel form, from an EndocrinoLogy 141:505-512(2000).

-i- FUNCTION: STIMULATES THE SECRETION OF FUNCTION: STIMULATES THE SECRETION OF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
                     Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1
Hormone; Amidation; Hypotl
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=30724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RH III) (LULIBERIN III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002012; -.
Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
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                                                                                     InterPro; IPR002012;
                                                                                                             -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EHWSYGLRPG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QHWSHGLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amidation; Hypothalamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
  AA;
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1230 MW; 284E
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Craniata; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 13
Pred. No. 0.023;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
284B20B72871F5A3
  284B3233786B45A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata;
                                                                                                                 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clupeomorpha; Clupeidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; E Clupeomorpha;
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a; Clupeidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GNRH-III) (LH-
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Best L
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=99312119; PubMed=10385393;

Won Schalburg K.R., Sherwood N.M.;

Von Schalburg K.R., Sherwood N.M.;

Regulation and expression of gonadotropin-releasing differs in brain and gonads in rainbow trout.";

Endocrinology 140:3012-3024(1999).
                                                                                                                                                                                                                                                                                                                                                            I SIMILARITY: TO THE GNRH EMBL; AF110993; AAD43463.1; InterPro; IPRO02012; - Pfam; PF00446; GnRH; 1. PROSITE; PS00473; GNRH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

YON Schalburg K.R., Sherwood N.M.;

YON Schalburg K.R., Sherwood N.M.;

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LULIBERIN)
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorh NCBI_TaxID=8022;
                                                                                   O9PT34 PRELIMINARY; PRT; 33 AA.

G9PT34;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
GONADOLIBERIN (GONADOTROPIN-RELEASING HORMON
(LULIBERIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                     Amidation;
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7; Conserv
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                                                                                                                                                                                                                                                                                Score 47; DB 1
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                099C825E4A72A3BB CRC64;
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No.
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HORMONE) (GNRH)
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0.051;
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                                 Oncorhynchus
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                                                          Euteleostomi;
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RESULT
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Best Local S
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MEDLINE-99312119; PubMed=10385393;
Von Schalburg K.R., Sherwood N.M.;
Von Schalburg K.R., Sherwood N.M.;
Regulation and expression of gonadotropin-releasing hormone 'Regulation and gonads in rainbow trout.";
differs in brain and gonads in rainbow trout.";
Endocrinology 140:3012-3024(1999).
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InterPro;
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yon Schalburg K.R., Sherwood N.M.;
yon Schalburg K.R., Sherwood N.M.;
submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
yi- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
                                                                                 -!- FUNCYLON. TO THE GNKH
-!- SIMILARITY TO THE SMKH-
EMBL; D31868; BAA06666.1; -
InterPro; IPR002012; -
InterPro; IPR002047; -
InterPro; IPR002047; -
InterPro; IPR00466; GnRH; 1.....
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-!- SIMILARITY: TO THE GNRH
EMBL; AF110533; AAD43461.1;
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Protacanthopterygii; Salmoniformes; Salmy
NCBL_TaxID-8023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pfam; PF00446; GnRH; 1.
proDom; PD005116; -; 1.
pROSITE; PS00256; AKH; UNKNOWN_1.
pROSITE; PS0473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002047;
                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GONADOLIBERIN PRECURSOR (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=NIKKO; TISSUE-BRAIN;
MEDLINE=96020547; PubMed=8546809;
                                                                                                                                                                                                                                                                                                                            (LULIBERIN)
                                                           PROSITE;
PROSITE;
                                                                                                                                                                                    Ashihara M., Suzuki M., Kubokawa K., Yoshiura
Urano A., Aida K.;
            SIGNAL
CHAIN
CHAIN
                                                                                                                                                   releasing hormone exist in salmo
J. Mol. Endocrinol. 15:1-9(1995)
                                                                                                                                                                          "Two differing precursor genes
 SEQUENCE
                                              Amidation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EHWSYGLRPG 10
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                                                                                                                                         FUNCTION: STIMULATES THE SECRETION OF
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                                                           PS00256; AKH; UNKNOWN_1.
PS00473; GNRH; 1.
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                                                 Hormone;
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    ĀΑ;
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3741 MW;
      9126
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33
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                                                                                                                                 GNRH FAMILY
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                                                                                                                                                                    salmonids.";
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      GNRH-ASSOCIATED PEPTIDE C64044EA521B2B8B CRC64;
                             GNRH
                                        POTENTIAL.
                                                                                                                                                                                for the
                                                                                                                                                                                                                                                                            Salmonidae; Oncorhynchus.
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                                                                                                                                                                                salmon-type
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                                                                                                                                                                                                                                                                                      Vertebrata;
Euteleostei
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                                                                                                                                                GONADOTROPINS
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RRN OCCOORDINATION
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Matches 7
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Best Local Similarity
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GONADOLLBERIN (GONADOTROPIN-RELEASING HORMONE) (GNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Von Schalburg K.R., Sherwood N.M.; "Regulation and expression of gonadotropin-releasing differs in brain and gonads in rainbow trout."; Endocrinology 140:3012-3024(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
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                                Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncor NCBI_TaxID-8022;
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SEQUENCE
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PROSITE; PS00256; AKH; UNKNOWN_1
PROSITE; PS00473; GNRH; 1.
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SEQUENCE FROM N.A
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Von Schalburg K.R., Sherwood N.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Pred. No. 0.
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0.47;
                                                                                                         Vertebrata; Euteleostomi;
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RESULT
Q9PSY9
ID Q0
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Q918P9
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Best Local S
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Best Local 9
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 01-MAY-2000
01-MAY-2000
01-MAR-2001
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Q918P9;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferriere F., Bailhache T., Jego P.;
"Oncorhynchus mykiss SGNRH-I cDNA from brain.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
SIMILARITY).
                              Q9PSY9
                                                                                                                                                                                                                                  FETTISSUE-BRAIN;
Fetriere F., Bailhache T., Jego P.;
Fetriere F., Bailhache T., Jego P.;
"Oncorhynchus mykiss sGnRH-II cDNA in the brain.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
SIMILARITY: TO THE GNRH FAMILY.
EMBL; AF232213; AAF91281.1; -.
                                                                                                                                                                                  PROSITE; PS00473; GNRH;
Amidation; Hormone.
SEQUENCE 82 AA; 9203
                                                                                                                                                                                                                                                                                                                                                         Oncorhynchus mykiss (Rainbow t
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                  GONADOLIBERIN (GONADOTROPIN-RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002047; -.
Pfam; PF00446; GnRH; 1.
PROSITE; PS00256; AKH; UNKNOWN_1.
PROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                InterPro; IPR002012; -. Pfam; PF00446; GnRH; 1.
                                                                                                                                                                                                                                                                                                                                      Protacanthopterygii;
NCBI_TaxID=8022;
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         (LULIBERIN).
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                                                                                                             1 EHWSYGLRPG
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                                                                                           QHWSYGWLPG
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82 AA;
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                  Conservative
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70
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                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                           Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                         trout) (Salmo gairdneri); Craniata; Vertebrata; E
Teleostei; Euteleostei;
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Pred.
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
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Page 6

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Search completed: November 13, 2001, 14:34:00 Job time: 426 sec
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Submitted (Feb-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (Feb-1998) to the EMBL/GenBank/DDBJ databases.

SUBMITTER STIMULATES THE SECRETION OF GONADOTROPINS (BY SIMILARITY).

C SIMILARITY: TO THE GNRH FAMILY.

C -!- SIMILARITY: TO THE GNRH FAMILY.

C -!- SIMILARITY: TO THE GNRH FAMILY.

REMBL; RAF046799; AADD2425.1; -.

                                                                                                                                                                                                                                                                                                                                                        Query Match 74.6
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
(LULIBERIN) (FRAGMENT).
Sparus aurata (Gilthead sea bream).
Sparus aurata (Gilthead sea bream).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Sparidae; Sparus.
NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=OVARY;
                                                                                                                                                                                                 1 EHWSYGLRPG 10
:||||| ||
24 QHWSYGWLPG 33
                                                                                                                                                                                                                                                                                                                                                                                                                    74.6%;
70.0%;
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